



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 164571

TO: Bao-Qun Li
Art Unit: 1648
Location: rem/3D24/3C18
Serial Number: 09/718803

Wednesday, April 12, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>.

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).



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78206
STIC-Biotech/ChemLib

184571 ME

From: Li, Bao-Qun
Sent: CRFT Friday, April 07, 2006 7:50 AM
To: STIC-Biotech/ChemLib
Subject: 09,718,803

Please do the sequence homology and interference search for SEQ.ID NO: 2 and 5. Thanks.

Bao Qun Li M.D
TC 1600
Art Unit 1648
Tel. 517-272-0904
REM, 3C18
Rm. 3D24

2aa 117
5aa 366

ME

Earlier date: 1999, 11-22

Paul, Shappner
Stephen Jaspers

Theresa Delsham
Paul D Bishop

1 check call adp
Patent
102 e info
2 interference reject

4/12
FBA

3

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGN

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:29:03 ; Search time 37.8882 Seconds
(without alignments)
929.454 Million cell updates/sec

Title: US-09-718-803A-5
Perfect score: 1905
Sequence: 1 MNATPSEEPGNLTADLD.....KLSTLKDESSRAWTESSINT 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461.5	24.2	424	JH0164	neurotensin recept
2	461.5	24.2	477	JC7913	capa receptor (CGI
3	460	24.1	418	S29506	neurotensin recept
4	440	23.1	595	JC8012	G protein-coupled
5	434.5	22.8	658	JC8011	neurotensin recept
6	413	21.7	418	A88013	protein K10B4.4 (i
7	405	21.3	416	S68832	neurotensin recept
8	390.5	20.5	380	S36143	kappa opioid recep
9	383.5	20.1	380	A48227	kappa opioid recep
10	379.5	19.9	380	JC2434	kappa opioid recep
11	375.5	19.7	380	A55259	kappa opioid recep
12	372.5	19.6	380	JC2338	kappa opioid recep
13	365.5	19.2	373	JC0087	delta opioid recep
14	359	18.8	367	JC2421	opioid receptor ho
15	359	18.8	367	I49022	kappa opioid recep
16	359	18.8	367	I56520	G protein-coupled
17	358.5	18.8	370	S43087	orphan opioid rece
18	357.5	18.8	392	S65693	opioid receptor mu
19	356	18.7	372	S34592	delta opioid recep
20	355	18.6	372	I48227	delta opioid recep
21	355	18.6	378	T15816	hypothetical prote
22	353.5	18.6	398	I56517	mu opioid receptor
23	352.5	18.5	400	I56553	mu opioid receptor
24	351.5	18.5	398	A57510	mu opiate receptor
25	351.5	18.5	398	I56504	mu opioid receptor
26	349	18.3	352	JE0296	thyrotropin releas
27	349	18.3	384	A47249	brain-specific som
28	347.5	18.2	372	I38532	delta opioid recep
29	343	18.0	384	JC4629	somatostatin recep

30	343	18.0	393	2	A39251	thyrotropin-releas
31	343	18.0	411	2	I56444	thyrotropin-relea
32	343	18.0	412	2	S23436	thyroliberin recep
33	340.5	17.9	388	2	JN0605	somatostatin recep
34	340.5	17.9	398	2	JN0708	thyrotropin-releas
35	339	17.8	519	2	S17783	tachykinin recepto
36	336	17.6	423	2	JC7677	allatostatin recep
37	329.5	17.3	362	2	JN0694	angiotensin II rec
38	327	17.2	425	2	T15959	hypothetical prote
39	321.5	16.9	345	2	S29248	somatostatin recep
40	320.5	16.8	387	2	JC5949	galanin receptor 2
41	320	16.8	363	2	I57955	somatostatin recep
42	320	16.8	364	2	JN0763	somatostatin recep
43	320	16.8	407	2	A34357	neurokinin 1 recep
44	320	16.8	427	2	S50150	gastric CCK-A rece
45	319	16.7	369	2	D41795	somatostatin recep

ALIGNMENTS

RESULT 1

JH0164
neurotensin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JH0164
R;Tanaka, K.; Masu, M.; Nakanishi, S.
Neuron 4, 847-854, 1990
A:Title: Structure and functional expression of the cloned rat neurotensin receptor.
A:Reference number: JH0164; MUID:90297956; PMID:1694443
A:Accession: JH0164
A:Molecule type: mRNA
A:Residues: 1-424 <TM>
A:Cross-references: UNIPROT:P20789; UNIPARC:UPI00001305AF
C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor. The
titer (neurotensin in the brain and as a hormone) cellular mediator in peripheral tis
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;65-87/Domain: transmembrane #status predicted <TM1>
F;97-121/Domain: transmembrane #status predicted <TM2>
F;144-165/Domain: transmembrane #status predicted <TM3>
F;189-210/Domain: transmembrane #status predicted <TM4>
F;236-260/Domain: transmembrane #status predicted <TM5>
F;309-330/Domain: transmembrane #status predicted <TM6>
F;348-372/Domain: transmembrane #status predicted <TM7>
F;4,38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.2%; Score 461.5; DB 2; Length 424;
Best Local Similarity 33.5%; Pred. No. 1.5e-32;
Matches 120; Conservative 67; Mismatches 120; Indels 51; Gaps 12;

Qy	3	NATPSEPGNLTADLDWDASPGNSLGDLELLQFPAPLAGVTATCTVALFVVVGIAGNL 62
Db	42	NTSESDTAGPN---SLLD-----VNTDIYSKVL-----VTATLALFVVVGTVGNS 83
Qy	63	LTMLVVSRR---FRELRTTNLYLSSWAFSDLLI-FLCMLPLDLVR-LWQYRPMWFGDLCK 117
Db	84	VTAFTRARKSLQSLQSTVHYHIGSLALSLLILLAMPVELYNFIWVHPWAPGAGCR 143
Qy	118	LFOVSESCYATVLTITALSVERFYFAICFPPLRAKVVTGRVKLVFIWVAVAFCSAGP 177
Db	144	GYFLRDACTYATALNVASLSVERYLAIChPFRAKTLMSRSRTKKFISAIWLASALLAIP 203
Qy	178	IFVLVGVHEH--NGTDPWDNECRPTFEFAVRSGLLTVMWVSSIPFPL-PVFCLTVLYSL 234
Db	204	MLFTMGLQNRSGDTHPGGL-VCTP---IVDTATVKVVIQVNTFMSELPFPLVSIILNTV 259
Qy	235	IGRKLWRRRGDAVVGASL-----RDONHKQTVKMLVAVVFAFIL 274
Db	260	IANKLTVMVHQAABQQRGVCTVGTTHNGLEHSTFNMTIEPGRVQALRGVLVRAVVIAPV 319
Qy	275	CWLPHFHVGRYLF8K-SFEPGSLBIAQISQYCNLVSFVLFYLSAAINPILYNIMSKYR 331

Qy 364 INT 366
Db 393 VRT 395

RESULT 5

JC8011
G protein-coupled neurotensin-2 receptor (CG8784) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: JC8011
R:Rosenkild, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; DeLotto, R.
Biochem. Biophys. Res. Commun. 309, 485-494, 2003
A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila
A:Reference number: JC8011; PMID: 12951076
A:Accession: JC8011
A:Molecule type: mRNA
A:Residues: 1-658 <ROS>
A:Cross-references: GB:AY277898
C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
development, diapause, feeding, and behavior.
C:Genetics:
A:Gene: c98784
A:Introns: 160/1; 215/2; 259/3; 326/1; 400/3
C:Keywords: G protein-coupled receptor; neurotensin-2 receptor; neurotensin; transmembrane protein

Query Match 22.8%; Score 434.5; DB 2; Length 658;
Best Local Similarity 34.9%; Pred. No. 5.2e-30;
Matches 129; Conservative 47; Mismatches 135; Indels 59; Gaps 12;
Qy 4 ATPSEEPG-----FNLTADLD-----WDASP-GNDSGLGDLQLF 38
Db 48 ANPSEPEMLLKNDKFLTHVAHLNITNENLNLGNTGNTASTMAADSPVDESILTR 107
Qy 39 PAPLAGVATCVAFVVGAGNLLTMLVSRFRELRTTNLYLSSMAFSDLLIFLC-MP 97
Db 108 TA-----LTVCYALIFVAGVLGNITCTIVSRNFMFTATNFYLFNLAVSDLLVSGIP 162
Qy 98 LDVRLWQYRPWNGDGLLCKLFQVSECTATVLTITLALSVRYFAICPPLRAKVVTK 157
Db 163 QELNLYWPDMPYTFDAMCINGSVLSEMANATVLTITAFVRYIACHPFRHTWSKL 222
Qy 158 GRVKLVIFVWAVAFCSAGPIFVLVGVHEN-GTDPMDTNECRPTFAVRSGLLTVMVW 216
Db 223 SRAIKTFIAWLAFLALPQAMQFSVYQYNEGYSCTWENDFYAHVAV-SGF----- 274
Qy 217 SSIFPFLPVCLTVLYSLIGRKLW-----RRGDVVGASLRDQNHQVTKVMLAV 269
Db 275 --IFGPGMTAICVLYLVLYGVKLRSLQLPRPTFDANRGLNAQG---RVIRMLVAV 328
Qy 269 VFAPILCWLPHVGRYLFPSKSPFGSLEIAQ--ISQYCNLVSF---VLFYLSAINEILY 323
Db 329 AVAFPLCWAPHAQLWAVYGLNINIGISKDAFNIDYFRILDYTSYGVLYFLSTCINPLLY 389
Qy 324 NIMSKYRVA 333
Db 389 NIMSKYRVA 398

RESULT 6

A88013
protein K1084.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A88013
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_elegans/
A:Accession: A88013

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <STO>
A:Cross-references: UNIPROT:O17239; UNIPARC:UPI000007537D; GB:chr_II; PIDN:AB71009.1; E
A:Note: similar to family 1 of G-protein coupled receptors
C:Genetics:
A:Gene: K1084.4
A:Map position: 2

Query Match 21.7%; Score 413; DB 2; Length 418;
Best Local Similarity 28.9%; Pred. No. 2.4e-26;
Matches 101; Conservative 71; Mismatches 114; Indels 64; Gaps 11;

Qy 44 AGVTATCV-----ALFVVGAGNLLTMLVSRFRELRTTNLYLSSMAFSDLL-IFLCMPL 98
Db 28 AGVIVPTVIIVGTIFLGLFGNICTCIVIAANKSMHNPNTNYVLSLAVSDIALLILGLPM 87
Qy 99 DLVRLWQYR-PWNGDGLLCKLFQVSECTATVLTITLALSVRYFAICPPLRAKVVTK 157
Db 88 EYQSLDYSPYRFRSEICARAFLEFTSYASIMICCFSEFWLAICHPLRSKIFSTL 147
Qy 158 GRVKLVIFVWAVAFCSAGPIFVLVGV-----HENGTDPMWT----- 195
Db 148 WRANVLIIILATISFVCLPIAFIVQINKLPEDAKYQWTKVSPFAVGLNRRFPV 207
Qy 196 -----NECRPTFAVRSGLLTVMVSSIFPFLPVCLTVLYSLIGRKLW 240
Db 208 STDGIFVLHTEFCAMNQSRPDQKQ-----IIIFATVFFVIPAIAIVIMYAHVAVLE 261
Qy 241 RRR-----RGDAVVGASLRDQNHQVTKVMLVAVVAFILCWLPHVGRVLFPSKSPFGSLEI 297
Db 262 SSETDLKGDQWV-KKRNKSNRTVLKMLSVITFTICWLPFHQRL---SVYTTWSET 317
Qy 298 AQISQYCNLVSVFLVYLS-----RAINPIYINIMSKYRVAVFR-LIG 339
Db 318 TTISPPVQFUSLMIVFYISGFCYYSNSAANPIYINILSQYRSAPFCRTILG 367

RESULT 7

S68822
neurotensin receptor 2, leucocabastine-sensitive - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C:Accession: S68822
R:Chalon, P.; Vica, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpech, B.; le Fur, G.; FEBS Lett. 385, 91-94, 1996
A:Title: Molecular cloning of a leucocabastine-sensitive neurotensin binding site.
A:Reference number: S68822; MUID:96228041; PMID:8647296
A:Accession: S68822
A:Molecule type: mRNA
A:Residues: 1-416 <CHA>
A:Cross-references: UNIPROT:Q63384; UNIPARC:UPI00001305B0; GB:X97121; NID:gl483579; PID
A:Experimental source: hypothalamus
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:33-58/Domain: transmembrane #status predicted <TM1>
F:70-91/Domain: transmembrane #status predicted <TM2>
F:110-131/Domain: transmembrane #status predicted <TM3>
F:155-175/Domain: transmembrane #status predicted <TM4>
F:204-230/Domain: transmembrane #status predicted <TM5>
F:296-315/Domain: transmembrane #status predicted <TM6>
F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 21.3%; Score 405; DB 2; Length 416;
Best Local Similarity 28.7%; Pred. No. 1.2e-27;
Matches 117; Conservative 68; Mismatches 160; Indels 62; Gaps 11;

Qy 2 WNATPSEPGFNITLADLDWADSPGNDLSGLDELQLPAPLAPLAVTATCVAFVVGAGN 61
Db 7 WPRPSPSAGLSL-----EARLGVDY-----RLWAKVLF---TALYSLIFAFGAGN 50
Qy 62 LLTMLVSRFRELRTTNLYLSSMAFSDLLIFLC-MPLDLVR-LWQYRPNWFGDGLLCKL 118

QY 134 ITALSVRYFAICFPLRAKVVVTKGRVKLVIFVWVAFCSAGPIFVLVGVHEHNGT--- 190
Db 149 LTMMSVDVRYIAVCHPVKALDFTPLKAKIINICIWLLA--SSVGISAIVLG-----GTVKVR 202
QY 191 DPWDTNECR---PTEFAVRSGLLTVMVWSSIFEFPLPVFCITVLVYSLIGRKLWRRRGD 246
Db 203 EDVDVIECSLQPPDDEYSWDLFMKICVFVFA--FVIFVLIIVCYITLM---ILRLKSVR 257
QY 247 AVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFFHVGRLYFSGSPFSGLEIAQISQYCNL 306
Db 258 LLGSRKRDRLRRITKLVLVAVVAFIICWTPPIHI--FILVEALGSTSHSTAALSSYYFC 315
QY 307 VSVFLFYLSAAINPILYNIMSKYRVAVFRLIGF-----EPFSQRLKSLTKDESS 356
Db 316 IA--LGYTNSSLNPLVYAFLDENFK-RCFRDPCFPPIKMRMERQSTNRVNTVQDPAS 369

RESULT 10

JC2434
kappa opioid receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: JC2434
R:Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.
Biochem. Biophys. Res. Commun. 205, 1353-1357, 1994
A:Title: Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor
A:Reference number: JC2434; MUID:95100967; PMID:7802669
A:Accession: JC2434
A:Molecule type: mRNA
A:Residues: 1-380 <NIS>
A:Cross-references: UNIPROT:P33534; UNIPARC:UPI000016CF1C; DDBJ:D31663
C:Genetics:
A:Map position: 1A2-3
A:Introns: 86/2; 204/1
C:Superfamily: vertebrate rhodopsin
C:Keywords: receptor

Query Match 19.9%; Score 379.5; DB 2; Length 380;
Best Local Similarity 26.9%; Pred. No. 1.8e-25;
Matches 98; Conservative 76; Mismatches 137; Indels 53; Gaps 10;
QY 20 DWDASPGNDSLGLDELQLFPA-----PLLAGVTATCVAFVVGIAGNLLTMLVVSRRPRE 73
Db 32 NMAESDSNGSVGSEDQQLSAHISPAIPVI--ITAVSVFVVGVLGNSLVMFVIIRYTK 89
QY 74 LRTTNLYLSSMAFSDLLIFLCMPDLVRLMQYRPWNFGDLLCKLFQVVSSECTYATVLT 133
Db 90 MKTATNIYIFNLADALVTTTTPQSA--VYLMSWPFPGDVLCKIVISIDYNNMFTSIFT 148
QY 134 ITALSVRYFAICFPLRAKVVVTKGRVKLVIFVWVAFCSAGPIFVLVGVHEHNGTDP- 192
Db 149 LTMMSVDVRYIAVCHPVKALDFTPLKAKIINICIWLLASSVGISAIVLGTVKVEDVDVI 208
QY 193 -----WDTECRTEFAVRSGLLTVMVWSSIFFPFVPLVCLTVLYSLIGRKL 239
Db 209 ECLLQFPDDDEYSWD-----LFMKICVVFVAFVPLVLIIVCYITLM---I 250
QY 240 WRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRLYFSGSPFSGLEIAQ 299
Db 251 LRLKSVRLSGSRKDRRLRRITKLVLVAVVAFIICWTPPIHI--FILVEALGSTSHSTAA 308
QY 300 ISOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLIGF-----EPFSQRLKSLTK 352
Db 309 LSSYYFCIA--LGYTNSSLNPLVYAFLDENFK-RCFRDPCFPPIKMRMERQSTNRVNTVQ 365
QY 353 DESS 356
Db 366 DPAS 369

RESULT 11

A55259
kappa opioid receptor - guinea pig

N:Alternate names: dynorphin receptor
C:Species: Cavia porcellus (guinea pig)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55259
R:Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Wats.
Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
A:Title: Primary structure and functional expression of a guinea pig kappa opioid (dyn.
A:Reference number: A55259; MUID:94224825; PMID:8170987
A:Accession: A55259
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-380 <XIE>
A:Cross-references: UNIPROT:P41144; UNIPARC:UPI0000130D98; GB:U04092; NID:G476106; PID:
C:Superfamily: vertebrate rhodopsin
C:Keywords: transmembrane protein

Query Match 19.7%; Score 375.5; DB 2; Length 380;
Best Local Similarity 28.4%; Pred. No. 4.1e-25;
Matches 92; Conservative 79; Mismatches 122; Indels 31; Gaps 11;
QY 21 WDASPGNDSLGLDELQLFPA-----PLLAGVTATCVAFVVGIAGNLLTMLVVSRRPREL 74
Db 33 WAEPDGNAGSAGPQDELEPAHISPAIPVI--ITAVSVFVVGVLGNSLVMFVIIRYTKM 90
QY 75 RTTNLYLSSMAFSDLLIFLCMPDLVRLMQYRPWNFGDLLCKLFQFVSESCYATVLT 134
Db 91 KTAITNIYIFNLADALVTTTTPQST--VYLMSWPFPGDVLCKIVISIDYNNMFTSIFT 149
QY 135 TALSVRYFAICFPLRAKVVVTKGRVKLVIFVWVAFCSAGPIFVLVGVHEHNGT---D 191
Db 150 TMSVDVRYIAVCHPVKALDFTPLKAKIINICIWLLS--SSVGISAIVLG-----GTVKRE 203
QY 192 PWDTECR---PTEFAVRSGLLTVMVWSSIFFPFVPLVCLTVLYSLIGRKLWRRRGDA 247
Db 204 DVDIIECSLQFPDDDYSDWDLFMKICVFVFA--FVIFVLIIVCYITLM---ILRLKSVRL 258
QY 248 VVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRLYFSGSPFSGLEIAQISOYCNLV 307
Db 259 LSGSRKDRRLRRITRLVLVAVVAFIICWTPPIHI--FILVEALGSTSHSTAALSSYYFCI 316
QY 308 SFVLFYLSAAINPILYNIMSKYR 331
Db 317 A--LGYTNSSLNPLVYAFLDENFK 338

RESULT 12

JC2338
kappa opioid receptor 1 - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: JC2338; A55354; I57005; G01546
R:Mansson, E.; Bare, L.; Yang, D.
Biochem. Biophys. Res. Commun. 202, 1431-1437, 1994
A:Title: Isolation of a human kappa opioid receptor cDNA from placenta.
A:Reference number: JC2338; MUID:94338360; PMID:8060324
A:Accession: JC2338
A:Molecule type: mRNA
A:Residues: 1-380 <MAN>
A:Cross-references: UNIPROT:P41145; UNIPARC:UPI00000001257; GB:U11053; NID:G532059; PIDN:
A:Experimental source: placenta
R:Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.
J. Biol. Chem. 269, 25966-25969, 1994
A:Title: Human kappa opiate receptor second extracellular loop elevates dynorphin's aff
A:Reference number: A55354; MUID:95014415; PMID:7929306
A:Accession: A55354
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 136-279 <MAN>
A:Cross-references: UNIPARC:UPI000016ABBA; GB:L36130; NID:G598184; PIDN:AAA63646.1; PID:
R:Zhu, J.; Chen, C.; Xue, J.
Life Sci. 56, 201-207, 1995
A:Title: Cloning of a human kappa opioid receptor from the brain.
A:Reference number: I57005


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Query Match      18.8%; Score 359; DB 2; Length 367;
Best Local Similarity 29.5%; Pred.No.1.le-23;
Matches          99; Conservative 70; Mismatches 120; Indels 44; Gaps 12;

QY   26  GNDSLGDELLQLPAPL-----AGVTATCVAFV-----GIAGNLLTWLVVS RF 71
DB   20  GNLSLNLTW---PHHLLLNASHAFPLGLKTVIGLYLAVCIIGGLGNCLVMYVL RH 76

QY   72  RELRTTNLYLSSMAFSDLLIFLCMPUL---DLVRLWQYRPWNFGDLLCKLFQFVSE SCTY 128
DB   77  TKMKTATNIYFNALADTLVLTLPQGTDILLGF----WPFGNALCKTVALDYNNMF 132

QY   129 ATVLTITALLSVERYFAICFLPRAKVVTKGRVKLVIFIWIAVAFCSAGPIFVLGVGEHEN 188
DB   133 TSTFTLTAMSDVRYVAICHPIRALDVRTSSKAQAVNAIWALASVVGVPVAIMSGAQVED 192

QY   189 GTDPMDTNECR---PTIEFAYRSGLLITVMWVSSIFFPELPVFCFLTIVLSYLGRKLRRRRRG 245
DB   193 -----BEIECLVIPAQDWGPVFACIIFLS--FIIPVLIISVCYSLMIRRL-----RG 241

QY   246 DAVV-GASLRDNKHOTVKMLAVVVFPAFICLWLPHFHVGRVLFKSFPSPGLETAIQISOYC 304
DB   242 VRLSSGSRKDRNLRRITRLVLVWVAVFGCWTVPQVFLVQGLGVQPGSETAAILRPC 301

QY   305 NLVSFVLYLSAAINPILYNIMSKYRVAVFR 336
DB   302 T-----ALGYVNSCLNPILYAFLDENFK-ACFR 328

```

Search completed: April 10, 2006, 17:34:31
Job time : 38.8882 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:23:48 ; Search time 65.646 Seconds
(without alignments)
783.099 Million cell updates/sec

Title: US-09-718-803A-2
Perfect score: 611
Sequence: 1 MPSGTVCSLLLGLMLDL.....LGKFLQILWEAKEAPADK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	100.0	117	2	AAW87991 Protein d
2	611	100.0	117	3	AAW87236 Human sig
3	611	100.0	117	4	AAW20101 Zsig33 pr
4	611	100.0	117	4	AAW62649 Human zsi
5	611	100.0	117	4	AAW38890 Human pol
6	611	100.0	117	4	AAW60511 Human ghr
7	611	100.0	117	5	AAW78319 Amino aci
8	611	100.0	117	5	AAW23838 Human zsi
9	611	100.0	117	5	AAW15883 Human zsi
10	611	100.0	117	6	AAW58046 Human PRO
11	611	100.0	117	6	AAW59124 Novel hum
12	611	100.0	117	6	AAW82636 Human sec
13	611	100.0	117	6	AAW17836 Novel hum
14	611	100.0	117	6	AAW60555 Human sec
15	611	100.0	117	6	AAW13937 Human PRO
16	611	100.0	117	6	AAW81090 Human PRO
17	611	100.0	117	6	AAW72522 Novel hum
18	611	100.0	117	6	AAW66790 Human PRO
19	611	100.0	117	6	AAW59871 Novel sec
20	611	100.0	117	6	AAW59271 Human sec
21	611	100.0	117	6	AAW25968 Human PRO
22	611	100.0	117	6	AAW25061 Human sec
23	611	100.0	117	6	AAW58977 Human sec
24	611	100.0	117	6	AAW92355 Novel hum

25	611	100.0	117	6	AAE33409 Human pre
26	611	100.0	117	6	ABU59420 Novel hum
27	611	100.0	117	6	ABU67066 Human sec
28	611	100.0	117	6	ABU92186 Novel hum
29	611	100.0	117	6	ABU10892 Human PRO
30	611	100.0	117	6	ABU81644 Novel hum
31	611	100.0	117	6	ABU88583 Human sec
32	611	100.0	117	6	ABO34097 Human PRO
33	611	100.0	117	6	ADA45961 Novel hum
34	611	100.0	117	6	ADA76392 Human PRO
35	611	100.0	117	6	ADA19042 Human PRO
36	611	100.0	117	6	ADA61665 Homo sapi
37	611	100.0	117	6	ADB19450 Novel hum
38	611	100.0	117	6	ADB27991 Human PRO
39	611	100.0	117	6	ADA86470 Novel hum
40	611	100.0	117	6	ADB16034 Human PRO
41	611	100.0	117	6	ADA37779 Human sec
42	611	100.0	117	6	ADA47820 Human PRO
43	611	100.0	117	6	ADA21465 Human sec
44	611	100.0	117	6	ADA10252 Human sec
45	611	100.0	117	6	ADA67615 Human PRO

ALIGNMENTS

RESULT 1
AAW87991
ID AAW87991 standard; protein; 117 AA.
XX AC AAW87991;
XX 07-APR-1999 (first entry)
XX Protein designated zsig33.
XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW nutrient absorption regulation; obesity; metabolic disorder.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note= "signal peptide"
FT Protein 24..117
FT Protein /note= "mature protein"
XX WO9842840-A1.
XX 01-OCT-1998.
XX 23-MAR-1998; 98WO-US005620.
XX 24-MAR-1997; 97US-0041102P.
XX 24-MAR-1997; 97US-00822897.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Deisher TA;
XX WPI; 1999-070071/06.
XX N-PSDB; AAX04550.
XX Human polypeptide having homology to motilin, zsig33 - useful e.g. to
PT treat gastrointestinal motility disorders, obesity etc. and to identify
PT antagonists to treat gastrointestinal hypermotility.
XX Claim 13; Page 55-56; 69pp; English.
XX The present sequence represents a protein designated Zsig33. The nucleic
CC acids are strongly expressed in stomach tissue. The polypeptide (or
CC allelic variants/orthologs) can be used to stimulate gastric motility,
CC measured as increased transit time or gastric emptying of an ingested

1.6

CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety or
 CC treat obesity and other metabolic disorders where neurological feedback
 CC modulates nutritional absorption. They are useful to identify zsig33
 CC agonists, antagonists and ligands and to produce antibodies
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPKLQPRALAGWLRLPE 60
 DB 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPKLQPRALAGWLRLPE 60
 QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQHSQALGKFLQDILWBEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQHSQALGKFLQDILWBEAKEAPADK 117

RESULT 2
 AAY87236
 ID AAY87236 standard; protein; 117 AA.
 XX
 AC AAY87236;
 DT 11-MAY-2000 (first entry)
 DE Human signal peptide containing protein HSP-13 SEQ ID NO:13.
 XX

KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antisthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.

OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US014484.
 XX
 PR 26-JUN-1998; 98US-0090762P.
 PR 31-JUL-1998; 98US-0094983P.
 PR 01-OCT-1998; 98US-0102686P.
 PR 11-DEC-1998; 98US-0112129P.
 XX
 PA (INCY) INCYTE PHARM INC.

XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akersblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 DR WPI: 2000-160673/14.
 DR N-PSDB; AAZ98121.

XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 PT disease.
 XX

PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
 CC used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
 CC or ribozyme therapeutics, for detecting related sequences or genetic
 CC variations, and for chromosomal mapping. HSP are also used to raise
 CC specific antibodies (Ab) and to screen for agonists and antagonists
 CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
 CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
 CC competitive drug screens, and for purification of HSP from natural
 CC sources
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 3; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPKLQPRALAGWLRLPE 60
 DB 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPKLQPRALAGWLRLPE 60
 QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQHSQALGKFLQDILWBEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQHSQALGKFLQDILWBEAKEAPADK 117

RESULT 3
 AAB20101
 ID AAB20101 standard; protein; 117 AA.
 XX
 AC AAB20101;
 DT 23-APR-2001 (first entry)
 DE Zsig33 protein.

XX SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue; therapy;
 KW human.
 XX Homo sapiens.
 OS
 FH Key
 FT Peptide 1..23
 FT /label= signal_peptide
 FT Protein 24..117
 FT /label= Mature_protein
 FT Peptide 24..34
 FT /label= SGIP_peptide
 FT /note= "this peptide is claimed in Claim 1"

XX WO200100830-A1.
 XX
 XX 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US018306.
 XX

```

PR 30-JUN-1999; 99US-00345157.
XX (ZYMO ) ZYMOGENETICS INC.
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2001-123010/13.
DR N-PSDB; AAF30033.
XX Novel variants of SGIP peptides for modulating contractility in duodenum
PT or jejunum tissue, pancreatic secretion of hormones and digestive
PT enzymes, inducing growth hormone secretion or modulating gastric
PT emptying.
XX
XX Disclosure; 54; 61pp; English.
XX
XX The present sequence is that of zsig33, a secreted protein with homology
CC to motilin (see AAB20102). Zsig33 is expressed at high levels in the
CC stomach, and at lower levels in the small intestine and pancreas. A novel
CC peptide fragment of zsig33, termed SGIP (see AAB20100), is claimed. SGIP
CC is a ligand for growth hormone secretagogue receptor, and is therefore
CC useful for modulating secretion of growth hormone and insulin like growth
CC factor 1. SGIP, and variant SGIP peptides, are used in claimed methods
CC for stimulating contractility in duodenum or jejunum tissue, modulating
CC pancreatic secretion of hormones and digestive enzymes, inducing growth
CC hormone secretion, and modulating gastric emptying
XX
XX Sequence 117 AA;
Query Match 100.0%; Score 611; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPSPTVCSLLLLGMLWLDLWLAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60
Db 1 MPSPTVCSLLLLGMLWLDLWLAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60
Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 4
AAB62649
ID AAB62649 standard; protein; 117 AA.
XX AAB62649;
AC AAB62649;
DT 23-JUL-2001 (first entry)
XX Human zsig33 polypeptide.
XX
XX zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
KW G-protein coupled receptor.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 24..37
FT /note= "specifically claimed fragment that binds to the
FT GHS-R"
XX
XX WO200138355-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US032074.
XX
XX 22-NOV-1999; 99US-0166765P.
XX

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PA (ZYMO ) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2001-355879/37.
DR N-PSDB; AAF83678.
XX Forming reversible peptide receptor complex for purifying cell and
PT peptides, stimulating signal transduction and modulating hormone
PT secretion, involves contacting a receptor with zsig33 polypeptide.
XX
XX Claim 1; Page 93-94; 11pp; English.
XX
XX The invention relates to a method of forming a reversible peptide-
CC receptor complex that involves providing an immobilized receptor, and
CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
CC is useful for purifying cells, purifying a peptide, stimulating signal
CC transduction in a cell expressing a receptor. It is also useful for
CC modulating secretion of hormones, neural development and/or utilization,
CC gastric contractility, nutrient uptake, secretion of digestive and
CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
CC hormone secretion in a mammal having a disease associated with abnormal
CC levels of growth hormone, such as osteoporosis, bone repair, bone
CC remodeling, low osteoblast levels, cartilage repair and remodeling,
CC skeletal dysplasia, immune suppression, obesity, growth retardation,
CC protein catabolic responses after surgery, cachexia, protein loss,
CC dwarfism, wound healing and ovulation induction, treating a mammal having
CC a metabolic disorder requiring neurological feedback, such as satiety
CC regulation, glucose absorption and metabolism and neuropathy-associated
CC gastrointestinal disorders, and stimulating glucose-induced insulin
CC release in a mammal. The present sequence represents the human zsig33
CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
XX
XX Sequence 117 AA;
Query Match 100.0%; Score 611; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPSPTVCSLLLLGMLWLDLWLAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60
Db 1 MPSPTVCSLLLLGMLWLDLWLAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60
Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 5
AAM38890
ID AAM38890 standard; protein; 117 AA.
XX AAM38890;
AC AAM38890;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2035.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX

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PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AAI58046.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 3; SEQ ID NO 2035; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAI36642-AAI42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKLQPRALAGWLRPE 60
Db 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKLQPRALAGWLRPE 60
QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 7
ABB78319
ID ABB78319 standard; protein; 117 AA.
XX
AC ABB78319;
XX
XX 05-DEC-2002 (first entry)
XX
DE Amino acid sequence of a human zsig33.
XX
KW Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note= "signal peptide"
FT 24..119
```

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PN WO200107475-A1.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-JP004907.
XX
PR 23-JUL-1999; 99JP-00210002.
PR 29-NOV-1999; 99JP-00338841.
PR 26-APR-2000; 2000JP-00126623.
XX
PA (KANG/) KANGAWA K.
XX
PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX
XX WPI: 2001-159704/16.
DR N-PSDB; AAF59645.
XX
PT New peptide compounds which induce growth hormone secretion and elevate
PT cell calcium concentrations, useful in treatment and diagnosis of infant
PT growth disorders.
XX
XX Claim 3; Page 182; 210pp; Japanese.
XX
CC The invention relates to a novel peptide compound or its salt which
CC induces the secretion of growth hormone and/or elevates calcium ion
CC concentration in cells. The peptides are ghrelin homologues and are
CC characterised in that at least one amino acid has been substituted by a
CC modified amino acid and/or a non-amino acid compound. The invention also
CC encompasses the unmodified peptides; the DNA encoding the peptides;
CC vectors and host cells comprising such DNA; a method of producing the
CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with no
CC accompanying side effects. The present sequence represents a ghrelin-type
CC growth hormone secretagogue (GHS) precursor protein of the invention
XX
SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKLQPRALAGWLRPE 60
Db 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKLQPRALAGWLRPE 60
QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 7
ABB78319
ID ABB78319 standard; protein; 117 AA.
XX
AC ABB78319;
XX
XX 05-DEC-2002 (first entry)
XX
DE Amino acid sequence of a human zsig33.
XX
KW Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note= "signal peptide"
FT 24..119
```

FT XX /note= "mature protein"

FN US6420521-B1.

XX 16-JUL-2002.

PD 30-JUN-2000; 2000US-00608810.

XX 30-JUN-1999; 99US-0141592P.

PR (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

PI WPI; 2002-634794/68.

XX N-PSDB; ABV72214.

DR New Short Gastrointestinal Peptide, which has homology to motilin, useful

PT for preventing, diagnosing and treating gastrointestinal disorders.

XX Disclosure; Col 39-40; 23pp; English.

PS The present sequence represents human zsig33. The specification describes

CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.

CC SGIP has homology to motilin. The SGIP peptide may be used in the

CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate SGIP expression. For example, SGIP may be used to treat

CC disorders associated with decreased expression by rectifying mutations or

CC deletions in a patient's genome that affect the activity of SGIP by

CC expressing inactive proteins or to supplement the patients own production

CC of SGIP. SGIP may also be used as an antigen in the production of

CC antibodies against SGIP and in assays to identify modulators of SGIP

CC expression and activity. The anti-SGIP antibodies, agonists and

CC antagonists may also be used to regulate expression and activity. The

CC anti-SGIP antibodies may also be used as diagnostic agents for detecting

CC the presence of SGIP in samples

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 5; Length 117;

Best Local Similarity 100.0%; Pred. No. 4e-59;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60

Db 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60

Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 8

AAE23838

ID AAE23838 standard; protein; 117 AA.

XX AAE23838;

AC AAE23838;

XX 10-SEP-2002 (first entry)

DT Human zsig33 protein.

DE Human; zsig33-like peptide; gastric contractility; nutrient uptake;

XX growth hormone; digestive enzyme; restorative therapy; gene therapy;

XX protein therapy; gastrointestinal; endocrine; anabolic.

OS Homo sapiens.

XX US2002055156-A1.

PN 09-MAY-2002.

PD 10-MAY-2001; 2001US-00853253.

PF

XX 11-MAY-2000; 2000US-0203300P.

PR (JASP/) JASPERS S R.

PA (SHEP/) SHEPPARD P O.

PA (DEIS/) DEISHER T A.

PA (BISH/) BISHOP P D.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

DR N-PSDB; AAD38238.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of

PT digestive/pancreatic enzymes and hormones.

XX Disclosure; Page 27; 34pp; English.

XX The invention relates to zsig33-like peptides and their corresponding

CC nucleic acids and methods for modulating gastric contractility, nutrient

CC uptake, growth hormones, secretion of digestive enzymes and hormones. The

CC sequences of the invention are used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate ZSIG33 expression.

CC The nucleic acids of the invention and their complements are used as DNA

CC probes in diagnostic assays to detect and quantitate the presence of

CC similar nucleic acids in samples, and therefore which patients may be in

CC need of restorative therapy. The ZSIG33 peptides are used as antigens in

CC the production of antibodies against ZSIG33 and in assays to identify

CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies

CC and antagonists are used to down regulate expression and activity. The

CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting

CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent

CC assay (ELISA)). The peptides and nucleic acids of the invention are used

CC to modulate gastric contractility, nutrient uptake, growth hormones, the

CC secretion of digestive enzymes and hormones, and/or secretion of enzymes

CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy

CC and zsig33-like peptide is used in protein therapy. The present sequence

CC is human zsig33 protein

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 5; Length 117;

Best Local Similarity 100.0%; Pred. No. 4e-59;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60

Db 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60

Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 9

AAE15883

ID AAE15883 standard; protein; 117 AA.

XX AAE15883;

AC AAE15883;

XX 26-MAR-2002 (first entry)

DT Human zsig33 protein.

DE Human; zsig33-like peptide; ZS33LP; immunity; developmental process;

XX infection; human immunodeficiency virus; vaccine; antihypoglycaemic;

XX adsorption enhancer; gastrointestinal disease; growth related disease;

XX inflammation; gene therapy; growth regulation; blood vessel formation;

XX HIV; zsig33 protein.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /label= Signal_peptide
FT 24..117
/note= "Human mature zsig33 protein"

XX WO200187933-A2.

XX 22-NOV-2001.

XX 10-MAY-2001; 2001WO-US015091.

XX 11-MAY-2000; 2000US-00569271.

XX (ZYMO) ZYMOGENETICS INC.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI: 2002-082982/11.

XX N-PSDB; AAD25759.

XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and treating
PT gastrointestinal and growth related diseases, comprises zsig33-like
PT peptides.

XX Disclosure; Page 80-81; 89pp; English.

CC The invention relates to zsig33-like peptides (ZS33LP) including zsig33-
CC linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon
CC peptides and nucleic acid molecules encoding such zsig33-like peptides.
CC ZS33LP peptides activate the immune system in boosting immunity to
CC infectious diseases, treating immunocompromised patients such as human
CC immunodeficiency virus (HIV) patients, in improving vaccines and in
CC treatment of bacterial, viral, protozoal and fungal infections. Peptides
CC of the invention are used to identify and isolate receptors involved in
CC growth regulation in the liver, blood vessel formation and other
CC developmental processes. They are useful for evaluating functions of
CC hypothalamus-pituitary-adrenal axis, to modulate growth and/or
CC differentiation of tumour cells, as additives to anti- hypoglycaemic
CC preparations containing glucose and as adsorption enhancers for oral
CC drugs which require fast nutrient action and to stimulate glucose-induced
CC insulin release. They are also useful as research reagents for the
CC expansion, differentiation, growth factor and hormone secretion and/or
CC cell-cell interactions of tissues associated with gastrointestinal
CC system, brain and central nervous system. These molecules are useful for
CC treating dysfunction associated with contractile tissues or to suppress
CC or enhance contractility in vivo and to treat gastrointestinal and growth
CC related diseases. ZS33LP peptides, nucleic acids and/or antibodies are
CC useful for treating disorders associated with gastrointestinal
CC contractility, secretion of digestive enzymes, hormone and acids,
CC secretion of hormones in the pancreas and/or brain, gastrointestinal
CC motility, recruitment of digestive enzymes, inflammation and regulation
CC of nutrient absorption. Sequences of the invention are useful in gene
CC therapy. The present sequence is human zsig33 protein

XX Sequence 117 AA;

Query Match 100.0%; Score 611; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLLLGMLWLDLWAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60

Db 1 MSPSGTVCSSLLLLGMLWLDLWAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLRLPE 60

QY 61 DGGQAGAEDELEVRNPDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRNPDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 10
ABU58046

ID ABU58046 standard; protein; 117 AA.
XX
AC ABU58046;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #78.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
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PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
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PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
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PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
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PR 22-JUN-1998; 98US-0090246P.
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PR 22-JUN-1998; 98US-0090254P.
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PR 23-JUN-1998; 98US-0090355P.
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PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090433P.
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PR 24-JUN-1998; 98US-0090472P.
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PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
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PR 26-JUN-1998; 98US-0090862P.
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PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
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PR 02-JUL-1998; 98US-0091633P.
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PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
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PR 18-AUG-1998; 98US-0097022P.
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PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.

PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
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PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 07-OCT-1998; 98US-0100858P.
PR 01-DEC-1998; 98US-0100858P.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-0113296P.
PR 08-MAR-1999; 98US-0113296P.
PR 12-MAR-1999; 98US-0113296P.
PR 02-JUN-1999; 98US-0113296P.
PR 23-JUN-1999; 98US-0113296P.
PR 07-JUL-1999; 98US-0113296P.
PR 20-JUL-1999; 98US-0113296P.
PR 26-JUL-1999; 98US-0113296P.
PR 28-JUL-1999; 98US-0113296P.
PR 17-AUG-1999; 98US-0113296P.
PR 15-SEP-1999; 98US-0113296P.
PR 15-SEP-1999; 98US-0113296P.
PR 30-OCT-1999; 98US-0113296P.
PR 08-NOV-1999; 98US-0113296P.
PR 01-DEC-1999; 98US-0113296P.
PR 16-DEC-1999; 98US-0113296P.
PR 20-DEC-1999; 98US-0113296P.
PR 05-JAN-2000; 98US-0113296P.
PR 06-JAN-2000; 98US-0113296P.
PR 11-FEB-2000; 98US-0113296P.
PR 18-FEB-2000; 98US-0113296P.
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PR 24-FEB-2000; 98US-0113296P.
PR 24-FEB-2000; 98US-0113296P.
PR 02-MAR-2000; 98US-0113296P.
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PR 15-MAR-2000; 98US-0113296P.
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PR 15-MAY-2000; 98US-0113296P.
PR 17-MAY-2000; 98US-0113296P.
PR 22-MAY-2000; 98US-0113296P.
PR 02-JUN-2000; 98US-0113296P.
PR 23-JUN-2000; 98US-0113296P.
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PR 11-AUG-2000; 98US-0113296P.
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PR 07-SEP-2000; 98US-0113296P.

Query Match 100.0%; Score 611; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQRVQQRKSKKPPAKLQPRALAGWLRLPE 60
Db 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQRVQQRKSKKPPAKLQPRALAGWLRLPE 60
Qy 61 DGGQAGAEDELEVRFNAPFDVGITKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGITKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 11
ABU59124
ID ABU59124 standard; protein; 117 AA.
XX
AC ABU59124;

XX 28-APR-2003 (first entry)
 XX Novel human secreted or transmembrane protein PRO1066.
 XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 XX US2002132252-A1.
 XX
 XX 19-SEP-2002.
 XX
 XX 14-NOV-2001; 2001US-00990442.
 XX 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
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 PR 04-JUN-1998; 98US-0088030P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.
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 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
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 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
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 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.

PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Klijavin JJ, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;
 XX
 XX WPI; 2003-247083/24.
 XX N-PSDB; ABX80294.
 XX
 XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments.
 XX
 XX Claim 12; Fig 186; 648pp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be

CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO112 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells [PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells] and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with,
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This is the
 CC amino acid sequence of a novel human PRO protein
 XX
 XX Sequence 117 AA;

Query Match 100.0%; Score 611; DB 6; Length 117;

Best Local Similarity 100.0%; Pred. No. 4e-59; Mismatches 0; Indels 0; Gaps 0;
 Matches 117; Conservative 0;

Qy 1 MPSPTVCSLLLLGLWLDLDMAGSSFLSPHQVQVKESKPKAKLPKALAGWLPE 60

Db 1 MPSPTVCSLLLLGLWLDLDMAGSSFLSPHQVQVKESKPKAKLPKALAGWLPE 60

Qy 61 DGGQAEAGDELEVRFNAPFDVGIKLGVQVQHSQALGKFLQDILMEEAKEAPADK 117

Db 61 DGGQAEAGDELEVRFNAPFDVGIKLGVQVQHSQALGKFLQDILMEEAKEAPADK 117

RESULT 12

ABU82636

ID ABU82636 standard; protein; 117 AA.

XX AC ABU82636;

XX DT 26-JUN-2003 (first entry)

XX DE Human secreted/transmembrane protein PRO1066.

XX KW Human; PRO: secreted protein; transmembrane protein;
 KW cardiac insufficiency disorders; angiogenesis; wound healing;
 KW cancerous tumour; immune response; retinal disorder; sight loss;
 KW retinitis pigmentosa; age-related macular degeneration; AMD;
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
 KW Crohn's disease; sports injury; arthritis.

XX OS Homo sapiens.

XX PN US2003032023-A1.

XX PD 13-FEB-2003.

XX PF 14-NOV-2001; 2001US-00990711.

XX PR 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 25-FEB-1998; 98US-0075945P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 28-APR-1998; 98US-0083322P.

XX PR 07-MAY-1998; 98US-0084600P.

XX PR 28-MAY-1998; 98US-0087106P.

XX PR 02-JUN-1998; 98US-0087607P.

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PR 07-OCT-1998; 98WO-US021141.
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PR 05-JAN-1999; 99WO-US000106.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
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PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
Query Match 100.0%; Score 611; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MPSPGTVCSSLLGLMLDLAMAGSFLSPHQRVQQRKSKPPAKLPRLAGWLREP 60
QY 61 DGGQAGAEDELEVRFNAPFDVGKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
DB 61 DGGQAGAEDELEVRFNAPFDVGKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 13
ABOI7836
ID ABOI7836 standard; protein; 117 AA.
XX
AC ABOI7836;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1066.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
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PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
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AC ABU60555;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #108.
XX
KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-0092599.
XX
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PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
XX

PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
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PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
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PR 30-MAY-2000; 2000WO-US014941.
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PR 28-FEB-2001; 2001WO-US006520.
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PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;
PI Zhang Z;
XX
WPI; 2003-288106/28.
DR N-PSDB; ABX90272.
XX
DR New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes.
XX
XX Claim 12; Fig 186; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-59;
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QY 1 MPSPTVCSLLILGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLQPRALAGWLKPE 60
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QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQVQOHSOALGKFLQDILWEEAKEAPADK 117
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RESULT 15
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 ID ABU13937 standard; protein; 117 AA.
 XX
 AC ABU13937;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Human PRO1066 polypeptide.
 XX
 KW Human; PRO polypeptide; secreted protein; transmembrane protein;
 KW Genetic disorder; antibacterial; immunosuppressive.
 XX
 OS Homo sapiens.
 XX
 XN US2002103125-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 20-NOV-2001; 2001US-00989731.
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 PR 28-MAY-1998; 98US-0087106P.
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 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
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 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAY-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUL-2001; 2001WO-US021066.
 PR 09-AUG-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH LTD.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;

XX WPI; 2003-102117/09.
 XX N-PSDB; ABX64118.

PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 12; Fig 186; 649pp; English.

XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for for
 CC identifying agonists or antagonists. The polynucleotide sequences
 CC encoding PRO polypeptides are useful as hybridisation probes, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC in the preparation of PRO polypeptides, for generating transgenic animals
 CC or knockout animals, to construct hybridisation probes for mapping the
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome markers, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. ABU13860-
 CC ABU14006 represent the human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly
 CC from the USPTO web site at seqdata.uspto.gov/psipsIDEntry.html
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPGTVCSSLLLLGLMLDLAMAGSSFLSPHQRVQQRKESKPPAKLOPRALAGWLRPE 60
 DB 1 MPSPGTVCSSLLLLGLMLDLAMAGSSFLSPHQRVQQRKESKPPAKLOPRALAGWLRPE 60
 QY 61 DGGQAGGADELEVRFPDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAGGADELEVRFPDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117

Search completed: April 10, 2006, 17:28:37
 Job time : 67.646 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:29:03 ; Search time 12.1118 Seconds
(without alignments)
929.454 Million cell updates/sec

Title: US-09-718-803A-2
Perfect score: 611
Sequence: 1 MPSPGTVCSSLLGLMLDL.....LGKFLQDLWEAKEAPADK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	100.0	117	1 A59316	ghrelin precursor
2	518	84.8	117	1 B59316	ghrelin precursor
3	88.5	14.5	115	1 A33323	motilin precursor
4	86	14.1	119	1 MPSFG	motilin precursor
5	79	12.9	1234	2 T30150	hypothetical prote
6	75.5	12.4	410	2 C84205	hypothetical prote
7	73.5	12.0	709	2 D82825	conserved hypothet
8	72.5	11.9	115	2 JC6511	motilin precursor
9	72.5	11.9	482	1 S03904	platelet-derived e
10	72.5	11.9	922	2 G83109	probable two-compo
11	72	11.8	147	2 T09722	histone H2B1 - upl
12	71	11.6	299	2 B36134	RepC protein - Esc
13	70	11.5	840	2 F90788	probable outer mem
14	70	11.5	840	2 G85648	probable usher pro
15	69	11.3	411	2 S47436	flagellar antigen
16	69	11.3	792	2 JC7122	protein kinase (EC
17	69	11.3	2273	2 T46477	calcium channel BI
18	69	11.3	2424	2 T46480	calcium channel BI
19	68.5	11.2	133	1 S24315	motilin precursor
20	68.5	11.2	340	2 S53763	homeotic protein H
21	68.5	11.2	330	2 AC0414	probable exported
22	68	11.1	533	2 A82252	beta-hexosaminidas
23	68	11.1	409	2 D87426	cyclopropane-fatty
24	67.5	11.0	270	2 E87408	hypothetical prote
25	67.5	11.0	416	2 T38428	T-complex protein
26	67.5	11.0	938	2 A13417	[glutamate-ammonia
27	67	11.0	233	2 T41263	hypothetical prote
28	67	11.0	2212	2 A41098	calcium channel pr
29	66.5	10.9	385	2 F70591	probable kefB prot

30	66.5	10.9	485	2 C75460	hypothetical prote
31	66.5	10.9	575	2 F86639	hypothetical prote
32	66.5	10.9	992	2 T08772	hypothetical prote
33	66.5	10.9	1018	2 T43168	hypothetical prote
34	66.5	10.9	1171	2 A50130	DNA-directed DNA p
35	66	10.8	247	2 S58394	myelin/oligodendro
36	66	10.8	770	2 A54444	DNA-binding protei
37	66	10.8	770	2 I49508	ISGF3 p91-related
38	66	10.8	922	2 D75615	excinuclease ABC c
39	65.5	10.7	262	2 D71068	probable pseudouri
40	65.5	10.7	334	2 S39870	transaldolase (EC
41	65.5	10.7	491	2 H97088	protein containing
42	65.5	10.7	627	2 T19542	hypothetical prote
43	65.5	10.7	692	2 AB0745	flagellar biosynth
44	65.5	10.7	692	2 B55546	flagellar biosynth
45	65.5	10.7	1065	2 B69795	acriflavin resista

ALIGNMENTS

RESULT 1

A59316
Ghrelin precursor - human
N;Alternate names: preproghrelin
C;Species: Homo sapiens (man)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Accession: A59316
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-117 <KOJ>
A;Cross-references: UNIPROT:Q9UBU3; UNIPARC:UPI00000362D3; GB:AB029434; NID:G6691571; I
A;Experimental source: tissue stomach endocrine cells
A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gro
C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;25/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 611; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKSKPPAKLOPRALAGWLPE	60
Db	1	MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKSKPPAKLOPRALAGWLPE	60
Qy	61	DGQGAEGAELEVRFNAPDVGIKLSGVQVQHSQALGKFLQDLILWEEAKEAPADK	117
Db	61	DGQGAEGAELEVRFNAPDVGIKLSGVQVQHSQALGKFLQDLILWEEAKEAPADK	117

RESULT 2

B59316
Ghrelin precursor - rat
N;Alternate names: preproghrelin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C;Accession: B59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Accession: B59316
A;Status: not compared with conceptual translation

A:Molecule type: mRNA; protein
A:Residues: 1-117 <XOU>
A:Cross-references: UNIPROT:Q9QYH7; UNIPARC:UPI000012B411; GB:AB029433; NID:g6691569; PI
A:Experimental source: strain SD; tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the stomach
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-25/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 84.8%; Score 518; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 4.1e-45;
Matches 97; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MPSPTGCSLLGLMLDLAMAGSSFLSPHQVQQRKESKKPPAKLPQPRALAGWLHPE 60
Db 1 MVSSATICSLLGLMLDMAMAGSSFLSPHQVQQRKESKKPPAKLPQPRALAGWLHPE 60

QY 61 DGGQAEAGAELEVRFPDFVGIKLSGVQYQHQHSGALGKFLQDILWEEAKEAPADK 117
Db 61 DRGQAEAEAELEIRFPDFVGIKLSGAQYQHQHSGALGKFLQDILWEEVKEAPANK 117

RESULT 3
A33323
motilin precursor - human
N:Contains: motilin; promotilin
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: A33323; S04489; S00156; A30329
R:Daikh, D.I.; Douglass, J.O.; Adelman, J.P.
DNA 8, 615-621, 1989
A:Title: Structure and expression of the human motilin gene.
A:Reference number: A33323; MUID:90091748; PMID:2574660
A:Accession: A33323
A:Molecule type: DNA
A:Residues: 1-115 <DAL>
A:Cross-references: UNIPROT:P12872; UNIPARC:UPI000012F3B4; GB:M30277; GB:M30278; GB:M30279
A:Note: The authors translated the codon CAG for residue 93 as Glu
R:Yano, H.; Seino, Y.; Fujita, J.; Yamada, Y.; Inagaki, N.; Takeda, J.; Bell, G.I.; Eddy
R:FSB Lett. 249, 248-252, 1989
A:Title: Exon-intron organization, expression, and chromosomal localization of the human
A:Reference number: S04489; MUID:89289989; PMID:2737284
A:Accession: S04489
A:Molecule type: DNA
A:Residues: 1-115 <YAN>
A:Cross-references: UNIPARC:UPI000012F3E4; EMBL:X15393; NID:g34691; PIDN:CAA33448.1; PID
R:Seino, Y.; Tanaka, K.; Takeda, J.; Takahashi, H.; Mitani, T.; Kurono, M.; Kayano, T.;
R:FSB Lett. 223, 74-76, 1987
A:Title: Sequence of an intestinal cDNA encoding human motilin precursor.
A:Reference number: S00156; MUID:88030048; PMID:3666144
A:Accession: S00156
A:Molecule type: mRNA
A:Residues: 1-115 <SET>
A:Cross-references: UNIPARC:UPI000012F3E4; EMBL:Y00695; NID:g34716; PIDN:CAA68690.1; PID
R:Dea, D.; Boileau, G.; Poitras, P.; Lahate, R.G.
Gastroenterology 96, 695-703, 1989
A:Title: Molecular heterogeneity of human motilinlike immunoreactivity explained by the
A:Reference number: A30329; MUID:89121385; PMID:2914635
A:Accession: A30329
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14, A' 16-113, 115 <DEA>
A:Cross-references: UNIPARC:UPI000017352E
C:Comment: This peptide hormone stimulates small intestinal muscle.
C:Genetics:
A:Gene: GDB:MLN
A:Cross-references: GDB:120187; OMIM:158270
A:Map position: 6p21.3-6p21.3
A:Introns: 39/3; 78/3; 113/1

C:Superfamily: motilin
C:Keywords: hormone
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-114/Product: promotilin #status predicted <PMAT>
F:26-47/Product: motilin #status predicted <MAT>
F:50-115/Domain: carboxyl-terminal propeptide #status predicted <CTP>

Query Match 14.5%; Score 88.5; DB 1; Length 115;
Best Local Similarity 25.4%; Pred. No. 0.076;
Matches 31; Conservative 29; Mismatches 41; Indels 21; Gaps 5;

QY 1 MPSPTGCSLLGLMLDLAMAGSS-----FLSPHQVQQRKESKKPPAKLPQPRAL 53
Db 1 MVSRKAAVALLVHVH-----AAMLASQTEAFVPIFYTGELQRMQEKERNG-----QKXSL 51

QY 54 AGWLRPEDGGQAEGA-----EDELE-VRFNAPFDVGIKLSGVQYQHQHSGALGKFLQDILWE 108
Db 52 SVWQSRSGEGPVPDPAEPIREENENIKLTAPELIGRMVNSRQLEKYVPATLEGLLSEMLPQ 111
QY 109 EA 110
Db 112 HA 113

RESULT 4
MSPG
motilin precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 #sequence revision 26-Jan-1996 #text_change 09-Jul-2004
A:Accession: A40932; A90748; A01578
R:Bond, C.T.; Millaver, G.; Godfrey, B.; Zimmerman, E.A.; Adelman, J.P.
Mol. Endocrinol. 2, 175-180, 1988
A:Title: Characterization of complementary deoxyribonucleic acid for precursor of porcine
A:Reference number: A40932; MUID:88288231; PMID:2456453
A:Accession: A40932
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <BON>
A:Cross-references: UNIPROT:P01307; UNIPARC:UPI00000362D4; GB:M31219; NID:g164589; PIDN:
A:Note: The authors translated the codon AGC for residue 29 as Ile
R:Brown, J.C.; Cook, M.A.; Dryburgh, J.R.
Can. J. Biochem. 51, 533-537, 1973
A:Title: Motilin, a gastric motor activity stimulating polypeptide: the complete amino
A:Reference number: A90748; MUID:73184120; PMID:4708633
A:Accession: A90748
A:Molecule type: protein
A:Residues: 26-28, I' 30-38, E' 40-47 <BRO>
A:Cross-references: UNIPARC:UPI000017352C
A:Experimental source: duodenal mucosa
R:Schubert, H.; Brown, J.C.
Can. J. Biochem. 52, 7-8, 1974
A:Title: Correction to the amino acid sequence of porcine motilin.
A:Reference number: A90749; MUID:74138109; PMID:4856583
A:Accession: A90749
A:Molecule type: protein
A:Residues: 38-41 <SCH>
A:Cross-references: UNIPARC:UPI000017352D
R:Yajima, H.; Kai, Y.; Kawatani, H.
J. Chem. Soc. Commun. 1975, 159-160, 1975
A:Title: Synthesis of the docosaepptide corresponding to the entire amino-acid sequence
A:Reference number: A92756
A:Contents: annotation
A:Note: a 22-residue peptide having the sequence and biological activity of the natural
R:Brown, J.C.; Mutt, V.; Dryburgh, J.R.
Can. J. Physiol. Pharmacol. 49, 399-405, 1971
A:Title: The further purification of motilin, a gastric motor activity stimulating poly
A:Reference number: A90755; MUID:72043589; PMID:4941085
A:Contents: annotation
A:Note: motilin, injected intravenously into dogs, stimulates motor activity in both ant
C:Superfamily: motilin
C:Keywords: duodenal mucosa; hormone; stomach
F:1-25/Domain: signal sequence #status predicted <SIG>

F;26-47/Product: motilin #status experimental <MAT>
F;50-119/Domain: carboxyl-terminal propeptide #status predicted <CTP>

Query Match 14.1%; Score 86; DB 1; Length 119;
Best Local Similarity 26.0%; Pred. No. 0.14;
Matches 20; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

QY 26 SFLSPHORVQORKEKPPAKLQPRALAGWLRPEDGGQAGAEDELEVRNAPFDVGK 85
DB 29 SFTYGELQRMQEKERKQKSLSVQQAASELGLPDPSEPTKEBERVVIKLLAPVDIGIR 88
QY 86 LSGVQYQOHSQALGKFL 102
DB 89 MDSRQLEKRYATLERLL 105

RESULT 5

T30160

hypothetical protein C37A2.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T30160

R;Le, T.T.; Kemp, K.; Scheet, P.

submitted to the EMBL Data Library, April 1997

A;Description: The sequence of C. elegans cosmid C37A2.

A;Reference number: Z20746

A;Accession: T30160

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1234 <LET>

A;Cross-references: UNIPROT:O01505; UNIPARC:UPI000017B91C; EMBL:U97194; PIDN:AAB52447.1;

A;Experimental source: strain Bristol N2; clone C37A2

C;Genetics:

A;Gene: CESP:C37A2.2

A;Map position: 1

A;Introns: 46/1; 124/1; 159/1; 231/1; 508/3; 740/3; 891/1; 931/1; 975/1; 1014/3; 1083/3

Query Match 12.9%; Score 79; DB 2; Length 1234;

Best Local Similarity 27.6%; Pred. No. 9.4;

Matches 32; Conservative 20; Mismatches 44; Indels 20; Gaps 6;

QY 2 PSPTVCSLLLLGMLWLDLWAGSSFLSPHORVQORKEKPPAKLQPRALAGWLRPED 61

DB 422 PQPG---SLGPMGSLGPTTAPPGSQPNPQQRIQQQQA-APASNSP-LLVNLSSNQ 476

QY 62 GGOAGAEDELEVRNAPFDVGKLSGV---QYQOHSQALGKFLQDILWEEAKEA 113

DB 477 PPQQ-----QYMPGPSAGLSMQQIAIQQQQHQQ-----YQQRILQQQQQQA 521

RESULT 6

C84205

hypothetical protein Vng0468c [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: C84205

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: C84205

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-410 <STO>

A;Cross-references: UNIPROT:Q9HS01; UNIPARC:UPI0000063639; GB:AB004437; NID:g10580073; F

C;Genetics:

A;Gene: VNG0468C

Query Match 12.4%; Score 75.5; DB 2; Length 410;

Best Local Similarity 30.3%; Pred. No. 6.3;

Matches 23; Conservative 9; Mismatches 37; Indels 7; Gaps 2;

QY 29 SPEHORVQORKEKPPAKLQPRALAGWLRPEDGGQAGAEDELEVRNAPFDVGKLSG 88

DB 78 SPHEYFQD-----QPGAVLEAFKQWL--VAAGEQCAEYRPEARVNNPITEGGEIVG 130

QY 89 VOYQOHSQALGKFLQD 104

DB 131 VKYGDDEYVGDIIID 146

RESULT 7

D82825

conserved hypothetical protein XF0277 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: D82825

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: D82825

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-709 <SIM>

A;Cross-references: UNIPROT:Q9PGM1; UNIPARC:UPI00000C2363; GB:AE003881; GB:AE003849; N

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,

as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froi

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lai

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF0277

Query Match 12.0%; Score 73.5; DB 2; Length 709;

Best Local Similarity 23.5%; Pred. No. 18;

Matches 36; Conservative 14; Mismatches 52; Indels 51; Gaps 6;

QY 5 GTVCSL-----LLIGMLWLDLWAGSSF----- 27

DB 422 GALASLIGFARLYLGAHWSLVGLGMLFGIFWLLVLGIAYRRRLTHELQVNPFLSWLFYGT 481

QY 28 -----LSPEHORVQORKEKPPAKLQPRALA--GWLRPEDGGQAGAEDELEVRNPA 78

DB 482 FSTAIAVMAPRHLEQKLTKEFPPPPS---PRAIAEGWKK-NDWRQLPARRNEFDAAERW 537

QY 79 PFDVGKLSGVQYQOHSQALGKFLQ-DILWEEA 110

DB 538 PLNVQAGSLVPLQQLHLETOGWRRQPTQGWKEA 570

RESULT 8

JC6511

motilin precursor - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C;Accession: JC6511

R;De Clercq, P.; Depoortere, I.; Peeters, T.

Gene 202, 187-191, 1997

A;Title: Isolation and sequencing of the cDNA encoding the motilin precursor from sheep

A;Reference number: JC6511; MUID:98087436; PMID:9427564

A;Accession: JC6511

RESULT 12

B36134
RepC protein - Escherichia coli plasmid TF-FC2
C:Species: Escherichia coli
C:Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 09-Jul-2004
C:Accession: B36134
R:Dorington, R.A.; Rawlings, D.E.
J. Bacteriol. 172, 5697-5705, 1990
A:Title: Characterization of the minimum replicon of the broad-host-range plasmid pTF-FC2
A:Reference number: A36134; MUID:91008941; PMID:2120189
A:Accession: B36134
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <DOR>
A:Cross-references: UNIPROT:Q03087; UNIPARC:UPI00000BE363; GB:M73777; GB:M35249; NID:g15
C:Genetics:
A:Genome: plasmid

Query Match 11.6%; Score 71; DB 2; Length 299;
Best Local Similarity 25.8%; Pred. No. 13;
Matches 25; Conservative 15; Mismatches 37; Indels 20; Gaps 4;

QY 32 HORVQQRKESK--KPPAKLQPRALAGWLRPEDGGQAE-----GAEDE-LEVRFN 77

DB 200 HTRINMAEVRKLETDPAKLLHQRUCGWDIDPKGSKAEIDTLCGYVWPDAANDAMKKRRQ 259

QY 78 APFDVGIKLGVQYQOHSQALGKFLQDILWEEAKEAP 114

DB 260 TARKALVELAAVGTVNEYAKGK-----WEISRPNP 290

RESULT 13

F90788
probable outer membrane usher protein ECs1278 [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F90788
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90788
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <HAY>
A:Cross-references: UNIPROT:Q8XAP8; UNIPARC:UPI00000D06A2; GB:BA000007; PIDN:BA034701.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs1278
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 50;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;

QY 3 SPGTVCSLLLGLMGLDLAMAGSFLSPHQVQORVKESKPPAKLQPR-----LAG 55

DB 127 APG-ITSQTQSLRLDLSVPQSLIS-----RPRGVVPPSELDTGASLAFMYIAN 177

QY 56 WLRPEDGGQAGAEDELEVRNAPFDVGIKLGVQYQOHSQALGKFLQDILWBEAK 111

DB 178 YYNVAYSGQNAHSQRSLSWASFN-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 14

G85648
probable usher protein Z1536 [imported] - Escherichia coli (strain O157:H7, substrain B1
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85648
R:Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
illier, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85648
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <STO>
A:Cross-references: UNIPROT:Q8XAP8; UNIPARC:UPI000016575F; GB:AE005174; NID:g12514401;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1536
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 50;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;

QY 3 SPGTVCSLLLGLMGLDLAMAGSFLSPHQVQORVKESKPPAKLQPR-----LAG 55

DB 127 APG-ITSQTQSLRLDLSVPQSLIS-----RPRGVVPPSELDTGASLAFMYIAN 177

QY 56 WLRPEDGGQAGAEDELEVRNAPFDVGIKLGVQYQOHSQALGKFLQDILWBEAK 111

DB 178 YYNVAYSGQNAHSQRSLSWASFN-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 15

S47436
flagellar antigen - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei
C:Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C:Accession: S47436

R:Imboden, M.; Mueller, N.; Hemphill, A.; Mattioli, X.Y.Z.; Seebeck, T.
submitted to the EMBL Data Library, August 1994

A:Description: Repetitive proteins from the flagellar cytoskeleton of African Trypanos

A:Reference number: S47436

A:Accession: S47436

A:Molecule type: mRNA

A:Residues: 1-411 <IMB>

A:Cross-references: UNIPROT:Q26766; UNIPARC:UPI000007CBBB; EMBL:Z36281; NID:g530358; P1

A:Experimental source: strain stock TREU 1285

C:Superfamily: cytoadherence-accessory protein hmw1

Query Match 11.3%; Score 69; DB 2; Length 411;
Best Local Similarity 30.2%; Pred. No. 29;
Matches 26; Conservative 16; Mismatches 28; Indels 16; Gaps 4;

QY 33 QRVQQRKESKPPAKLQPRALAGWLRPEDGGQAGAEDELEVRNAPFDVGIKLGVQYQ 92

DB 317 EALEELEEPQAPAEQAPEAVA---PE-GDIAVEALEELEEPQAP-----AEAQ 362

QY 93 QHSQALGKFLQDIL--WEEAKEAPAD 116

DB 363 PEAQPEGDTAVEALEELEEPQAPAE 388

Search completed: April 10, 2006, 17:34:30
Job time : 14.1118 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:33:53 ; Search time 16.472 Seconds
(without alignments)
587.240 Million cell updates/sec

Title: US-09-718-803A-2
Perfect score: 611
Sequence: 1 MPSGTCVCSLLGLMLDL.....LGKFLQDILMEAKEAPADK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	611	100.0	117	2	US-09-608-810A-4
4	611	100.0	117	2	US-09-404-417A-2
5	611	100.0	117	2	US-09-794-987-2
6	611	100.0	117	2	US-09-853-253-2
7	611	100.0	117	2	US-09-991-181-268
8	611	100.0	117	2	US-09-990-444-268
9	611	100.0	117	2	US-09-796-158-2
10	611	100.0	117	2	US-09-997-333-268
11	611	100.0	117	2	US-09-992-598-268
12	145	23.7	28	2	US-09-880-498-1
13	130	21.3	25	2	US-09-853-253-9
14	126	20.6	24	2	US-09-853-253-4
15	125	20.5	24	2	US-09-853-253-10
16	121	19.8	23	2	US-09-853-253-5
17	121	19.8	23	2	US-09-853-253-6
18	119	19.5	23	2	US-09-853-253-11
19	91	14.9	18	2	US-09-404-417A-11
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22	86	14.1	119	2	US-08-822-897C-4
23	86	14.1	119	2	US-09-608-810A-5
24	86	14.1	119	2	US-09-404-417A-4
25	86	14.1	119	2	US-09-794-987-4
26	86	14.1	119	2	US-09-796-158-4
27	85	13.9	16	2	US-09-853-253-15

28	85	13.9	16	2	US-09-853-253-16	Sequence 16, Appl
29	79	12.9	15	2	US-09-853-253-17	Sequence 17, Appl
30	76	12.4	15	2	US-09-853-253-25	Sequence 25, Appl
31	76	12.4	352	2	US-09-902-540-10277	Sequence 10277, A
32	73	11.9	323	2	US-08-028-213B-25	Sequence 25, Appl
33	72.5	11.9	244	1	US-08-696-827-1	Sequence 1, Appl
34	72.5	11.9	773	2	US-09-252-991A-23152	Sequence 23152, A
35	71.5	11.7	589	2	US-09-134-000C-5710	Sequence 5710, Ap
36	71	11.6	556	2	US-09-524-101D-22	Sequence 22, Appl
37	70	11.5	220	1	US-08-761-248B-4	Sequence 4, Appl
38	70	11.5	255	2	US-09-949-016-10591	Sequence 10591, A
39	69.5	11.4	247	2	US-09-252-991A-27419	Sequence 27419, A
40	69.5	11.4	341	2	US-09-252-991A-27327	Sequence 27327, A
41	69.5	11.4	667	2	US-09-902-540-15196	Sequence 15196, A
42	69	11.3	406	2	US-09-252-991A-28102	Sequence 28102, A
43	69	11.3	1088	2	US-09-130-242-2	Sequence 2, Appl
44	69	11.3	1088	2	US-09-583-610D-2	Sequence 2, Appl
45	69	11.3	1088	2	US-09-949-016-6935	Sequence 6935, Ap

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

different invertebrate


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;
; Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawielak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Query Match 100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLLGMLWLDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60
Db 1 MPSPTVCSLLLLGMLWLDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60

Qy 61 DGGQAEAGAELEVRFNAPFDVGKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGAELEVRFNAPFDVGKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 6
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zbg33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Query Match 100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 DGGQAEAGAELEVRFNAPFDVGKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
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RESULT 7
US-09-991-181-268
; Sequence 268, Application US/09991181
; Patent No. 6913419
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
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65	PRIOR APPLICATION NUMBER: 60/089599	66	PRIOR FILING DATE: 1998-07-02
66	PRIOR FILING DATE: 1998-06-17	67	PRIOR APPLICATION NUMBER: 60/091633
67	PRIOR APPLICATION NUMBER: 60/089600	68	PRIOR FILING DATE: 1998-07-02
68	PRIOR FILING DATE: 1998-06-17	69	PRIOR APPLICATION NUMBER: 60/091978
69	PRIOR APPLICATION NUMBER: 60/089653		


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Query Match      100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGMLDLAMAGSSFLSPHORVQORKEKSKPPAKLOPRALAGWLRLPE 60
DB 1 MPSPTVCSLLLLGMLDLAMAGSSFLSPHORVQORKEKSKPPAKLOPRALAGWLRLPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 8
US-09-990-444-268
; Sequence 268, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
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Query Match	100.0%;	Score 611;	DB 2;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 6.9e-67;		

	Query Match	100.0%;	Score 611;	DB 2;	Length 117;						
	Best Local Similarity	100.0%;	Pred. No. 6.9e-67;								
	Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;						
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Db	1	MPSPGTVC	LLLLLGM	LWLDM	LAGSSFLSP	EHQRVQ	QRKESK	KKPPAK	LQPRAL	AGMLRPE	60
Qy	61	DGQQAEG	ADELEVR	FNAP	DVGIK	LSGVQY	QOHSQ	ALGKFL	ODIL	WEEAKE	PADK 117
Db	61	DGQQAEG	ADELEVR	FNAP	DVGIK	LSGVQY	QOHSQ	ALGKFL	ODIL	WEEAKE	PADK 117

RESULT 10
US-09-997-333-268

; Sequence 268, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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[illegible]

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; PRIOR FILING DATE: 1998-06-22
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; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.9e-67;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSFGTVCSTLLGLMLDLAMAGSSFLSPFHQVQQRKSKPPAKLQPRALAGWL RPE 60

Db 1 MPSFGTVCSTLLGLMLDLAMAGSSFLSPFHQVQQRKSKPPAKLQPRALAGWL RPE 60

Qy 61 DGGQAGAEDELEVRFNAPFDVGILKSGVYQHQHSGALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRFNAPFDVGILKSGVYQHQHSGALGKFLQDILWEEAKEAPADK 117

RESULT 12

US-09-880-498-1

; Sequence 1, Application US/09880498

; Patent No. 6861409

; GENERAL INFORMATION:

; APPLICANT: Zentaris AG

; TITLE OF INVENTION: Growth Hormone Secretagogues

; FILE REFERENCE: 87264-100

; CURRENT APPLICATION NUMBER: US/09/880,498
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US Provisional Appln No. 6861409 60/234,928
; FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US Provisional Appln No. 6861409 60/211,326
; FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: rat
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: o-n-octanoyl
US-09-880-498-1

not relevant

Query Match 23.7%; Score 145; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-10; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

QY 24 GSSFLSPHEQRVQQRKESKPKLQPR 51
Db 1 GSSFLSPHEQRVQQRKESKPKLQPR 28

RESULT 13
US-09-853-253-9
; Sequence 9; Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-9

Query Match 21.3%; Score 130; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.2e-09; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 76 FNAPFDVGKLSGVQYQHQHSQLGK 100
Db 1 FNAPFDVGKLSGVQYQHQHSQLGK 25

RESULT 14
US-09-853-253-4
; Sequence 4; Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300

; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-4

Query Match 20.6%; Score 126; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-08; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 52 ALAGWLRPEDGGQAGAEDELEVR 75
Db 1 ALAGWLRPEDGGQAGAEDELEVR 24

RESULT 15
US-09-853-253-10
; Sequence 10; Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
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; ORGANISM: Homo sapiens
US-09-853-253-10

Query Match 20.5%; Score 125; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e-08; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

QY 76 FNAPFDVGKLSGVQYQHQHSQLG 99
Db 1 FNAPFDVGKLSGVQYQHQHSQLG 24

Search completed: April 10, 2006, 17:35:42
Job time : 17.472 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:24:12 ; Search time 70.4907 Seconds
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Title: US-09-718-803A-2

Perfect score: 611

Sequence: 1 MPSPGTVCSSLLGLMLDL.....LGKFLQDILWEEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	100.0	117	1	GHRL_HUMAN
2	591	96.7	117	2	Q6UDE7 MACMU
3	524	85.8	117	1	GHRL_MOUSE
4	518	84.8	117	1	GHRL_RAT
5	515	84.3	117	2	Q6CHF3 MERUN
6	511	83.6	117	1	GHRL_FELCA
7	476	77.9	117	1	GHRL_CANPA
8	472.5	77.3	118	1	GHRL_PIG
9	436.5	71.4	116	1	GHRL_CAPHI
10	422.5	69.1	116	2	Q6G3T0 SHEEP
11	417.5	68.3	116	1	GHRL_BOVIN
12	392	64.2	91	2	Q6YF88 HUMAN
13	370.5	60.6	97	2	Q6G3C6 SHEEP
14	325.5	53.3	78	2	Q7TSD1 MOUSE
15	320	52.4	86	2	Q81174 MOUSE
16	289.5	47.4	74	2	Q67B85 PIG
17	260	42.6	124	2	Q6F4B3 TRASC
18	249.5	40.8	116	2	Q6VMU7 PAVES
19	247.5	40.5	65	2	Q6TGF0 PIG
20	245.5	40.2	116	2	Q6VMU6 ANAPL
21	243.5	39.9	116	2	Q6VMU5 DRONO
22	232.5	38.1	116	2	Q7T1B9 MELGA
23	229.5	37.6	116	2	Q7T2V1 CHICK
24	229.5	37.6	116	2	Q6AV73 CHICK
25	211	34.5	114	2	Q6F4B4 TRASC
26	196.5	32.2	54	2	Q6SLF6 CEREL
27	195.5	32.0	54	2	Q6SLP2 ODOHE
28	195.5	32.0	54	2	Q6SLP8 RANTA
29	194.5	31.8	54	2	Q6SLG1 CAPHI
30	192.5	31.5	54	2	Q6SLF4 SCETA
31	190.5	31.2	52	2	Q6SLF9 OCETA

32	187	30.6	36	2	Q5Y392 HUMAN	Q5Y392 homo sapien
33	180.5	29.5	54	2	Q6SLG3 SHEEP	Q6SLG3 ovis aries
34	180.5	29.5	54	2	Q6SPC2 BISBI	Q6SPC2 bison bison
35	178.5	29.2	54	2	Q6SLG5 KGBR	Q6SLG5 kogia brevi
36	178.5	29.2	54	2	Q6SLG7 BOVIN	Q6SLG7 bos taurus
37	163	26.7	40	2	Q6TGB9 PIG	Q6TGB9 sus scrofa
38	146	23.9	111	1	GHRL_ANGUA	Q81FY4 anguilla ja
39	124	20.3	111	1	GHRL_ONCMY	Q761Q4 oncorhynch
40	117.5	19.2	108	2	Q4LET9 ICTPU	Q4LET9 ictalurus p
41	116.5	19.1	108	2	Q4LET8 ICTPU	Q4LET8 ictalurus p
42	112.5	18.4	35	2	Q6SPC3 ANAM	Q6SPC3 antilocapra
43	111	18.1	32	2	Q6SLF5 CEREL	Q6SLF5 cervus elap
44	110.5	18.1	107	2	Q4L142 ACASC	Q4L142 acanthopagr
45	102	16.7	29	2	Q6SLG2 SHEEP	Q6SLG2 ovis aries

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3, Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein) (Contains: Ghrelin-27; Ghrelin-28 (Ghrelin)).
DE Ghrelin-27; Ghrelin-28 (Ghrelin)).
GN Name=GHRL; Synonyms=MTLRP; ORFNames=UN0524/PRO1066;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND ACYLATION OF SER-26.
RC TISSUE=Stomach;
RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 24-33.
RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Wajnrajch M.P., Ten I.S., Gertner J.M., Leibel R.L.;
RT "Genomic organization of the human Ghrelin gene.";
RL J. Endocr. Genet. 1:231-233(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), TISSUE SPECIFICITY, ACYLATION OF SER-26, AND MASS SPECTROMETRY.
RC TISSUE=Stomach;
RX PubMed=12414809; DOI=10.1074/jbc.M205366200;
RA Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;
RT "Structural divergence of human ghrelin. Identification of multiple ghrelin-derived molecules produced by post-translational processing.";
RL J. Biol. Chem. 278:64-70(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wiewand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RL [6]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RP TISSUE=Blood;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [7]
RN PROTEIN SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RL [8]
RN REVIEW.
RP MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RX Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RA "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9UBU3-1; Sequences=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9UBU3-2; Sequences=VSP_003245;
CC -!- TISSUE SPECIFICITY: Highest level in stomach. All forms are found
CC in serum as well. Other tissues compensate for the loss of ghrelin
CC synthesis in the stomach following gastrectomy.
CC -!- PTM: O-n-octanoylation is essential for activity. The O-n-
CC decanoylated forms Ghrelin-27-C10 and Ghrelin-28-C10 differ in the
CC length of the carbon backbone of the carboxylic acid bound to Ser-
CC 26. A small fraction of ghrelin, ghrelin-28-C10:1, may be modified
CC with an unsaturated carboxylic acid.
CC -!- MASS SPECTROMETRY: MW=3398.9; MW ERR=0.3; METHOD=Electrospray;
CC RANGE=24-51 (Ghrelin-28-C10); NOTE=O-decanoylated form (Ref.4).
CC -!- MASS SPECTROMETRY: MW=3397.2; MW ERR=0.5; METHOD=Electrospray;
CC RANGE=24-51 (Ghrelin-28-C10:1); NOTE=O-decanoylated form (Ref.4).
CC -!- MASS SPECTROMETRY: MW=3371.3; MW ERR=0.1; METHOD=Electrospray;
CC RANGE=24-51 (Ghrelin-28); NOTE=O-octanoylated form (Ref.4).

CC -!- MASS SPECTROMETRY: MW=3243.6; MW ERR=0.4; METHOD=Electrospray;
CC RANGE=24-50 (Ghrelin-27-C10); NOTE=O-decanoylated form (Ref.4).
CC -!- MASS SPECTROMETRY: MW=3214.6; MW ERR=0.6; METHOD=Electrospray;
CC RANGE=24-50 (Ghrelin-27); NOTE=O-octanoylated form (Ref.4).
CC -!- SIMILARITY: Belongs to the motilin family.
CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/GhrelinID327.html".
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB029434; BAA89371.1; -; mRNA.
CC EMBL; AJ252278; CAB65733.1; -; mRNA.
CC EMBL; AF296558; AAG10300.1; -; Genomic_DNA.
CC EMBL; AB035700; BAB19045.1; -; mRNA.
CC EMBL; AY359053; AAO89412.1; -; mRNA.
CC EMBL; BC025791; AAH25791.1; -; mRNA.
CC PIR; A59316; A59316.
CC PDB; IPTX; Model; A=1-117.
CC Ensemble; ENSG00000157017; Homo sapiens.
CC H-InvDB; HIX0003050; -.
CC MIM; 605353; -.
CC GO; GO:0005615; C:extracellular space; ISS.
CC GO; GO:001664; F:G-protein-coupled receptor binding; ISS.
CC GO; GO:0016608; F:growth hormone-releasing hormone activity; ISS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; ISS.
CC GO; GO:00050791; P:regulation of physiological process; ISS.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin-ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC PANTHER; PTHR14122; Preproghrelin; 1.
CC Pfam; PF04643; Motilin_assoc; 1.
CC Pfam; PF04644; Motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin; 1.
CC 3D-structure; Alternative splicing; Direct protein sequencing;
CC Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23
FT PEPTIDE 24 51 Ghrelin-28.
FT PEPTIDE 24 50 Ghrelin-27.
FT PROPEP 52 117 Removed in mature form.
FT LIPID 26 26 O-decanoyl serine (in form ghrelin-27-C10
FT and form ghrelin-28-C10).
FT LIPID 26 26 O-octanoyl serine (in form ghrelin-27 and
FT form ghrelin-28).
FT VARSPLIC 37 37 Missing (in isoform 2).
FT CONFLICT 72 72 /FTId=VSP_003245.
FT SEQUENCE 117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
Query Match 100.0%; Score 611; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPGTVCSSLLLLGMLWLDLAWAGSSFLSPHEQRVQQRKESKKPPAKLPRLAGWL RPE 60
Db 1 MSPGTVCSSLLLLGMLWLDLAWAGSSFLSPHEQRVQQRKESKKPPAKLPRLAGWL RPE 60
QY 61 DGGQAGAEDELEVRFPDVGILSGVQVOOHSQALGKPLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFPDVGILSGVQVOOHSQALGKPLQDILWEEAKEAPADK 117
RESULT 2
ID Q6UDE7_MACMU PRELIMINARY; PRT; 117 AA.
AC Q6UDE7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)


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CC      -!- SIMILARITY: Belongs to the motilin family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AJ243503; CAB46500.1; -; mRNA.
CC      EMBL; AB035701; BAB19046.1; -; mRNA.
CC      EMBL; AB060078; BAB69857.1; -; Genomic_DNA.
CC      EMBL; AK008658; BAB25814.1; -; mRNA.
CC      EMBL; AK008860; BAB25934.1; -; mRNA.
CC      Ensembl; ENSMUSG0000064177; Mus musculus.
CC      MGI; MGI:1930008; Ghrl.
CC      GO; GO:0005737; Cytoplasm; IDA.
CC      GO; GO:0005615; Extracellular space; TAS.
CC      GO; GO:0005179; Hormone activity; TAS.
CC      InterPro; IPR006737; motilin_assoc.
CC      InterPro; IPR006738; motilin_ghrelin.
CC      InterPro; IPR005441; Preproghrelin.
CC      PANTHER; PTHR14122; Preproghrelin; 1.
CC      Pfam; PF04643; Motilin_assoc; 1.
CC      Pfam; PF04644; Motilin_ghrelin; 1.
CC      PRINTS; PR01624; GHRELIN.
CC      ProDom; PD132162; Preproghrelin; 1.
CC      Alternative splicing; Direct protein sequencing; Hormone; Lipoprotein;
KW      Signal.
FT      SIGNAL          1      23
FT      PEPTIDE         24      51
FT      PROPEP          52     117
FT      LIPID           26      26
FT      LIPID           26      26
FT      VARSPLIC        37      37
FT      Missing (in isoform 2).
FT      /FTID=VSP_003246.
SQ      SEQUENCE 117 AA; 13207 MW; EACE49D2E3CA7203 CRC64;

Query Match      85.8%; Score 524; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 8.9e-45;
Matches 98; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY      1  MPSPTVCSLLLGMLDLAMAGSFLSPHEHQVQQRKSKPKAKLPRLAGWLKPE 60
DB      1  MLSSGTICSLLLSLMWMAMAGSFLSPHEHQVQQRKSKPKAKLPRLAGWLKPE 60

QY      61  DGGQGAEGAELEVRFPFDVGIKLSGVQVQHSQALGKFLQDILWBEAKEAPADK 117
DB      61  DEGQAEETEELIRFPNPFVDVGIKLSGVQVQHSQALGKFLQDILWBEAKEAPADK 117

RESULT 4
GHR_L RAT
ID  _GHR_L RAT      STANDARD;      PRT;      117 AA.
AC  Q9QYH7; Q9ET69;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE  releasing peptide) (Motilin-related peptide).
GN  Name=Ghrl;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridea; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), PROTEIN SEQUENCE OF 24-51,
RP  MASS SPECTROMETRY, AND ACYLATION OF SER-26.
RC  STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX  MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
RA  Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
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RT      "Ghrelin is a growth-hormone-releasing acylated peptide from
RT      stomach.";
RL      Nature 402:656-660(1999).
RN      [2]
RP  NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF
RP  24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
RC  STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX  MEDLINE=20357315; PubMed=10801861; DOI=10.1074/jbc.M002784200;
RA  Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT      "Purification and characterization of rat des-Gln14-ghrelin, a second
RT      endogenous ligand for the growth hormone secretagogue receptor.";
RL      J. Biol. Chem. 275:21995-22000(2000).
RN      [3]
RP  CHARACTERIZATION.
RX  MEDLINE=21092536; PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
RA  Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT      "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
RT      in gastrointestinal tissue.";
RL      Biochem. Biophys. Res. Commun. 279:909-913(2000).
RN      [4]
RP  STRUCTURE-ACTIVITY RELATIONSHIP.
RX  MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553;
RA  Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
RA  Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
RT      "Structure-activity relationship of ghrelin: pharmacological study of
RT      ghrelin peptides.";
RL      Biochem. Biophys. Res. Commun. 287:142-146(2001).
RN      [5]
RP  REVIEW.
RX  MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA  Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT      "Ghrelin: discovery of the natural endogenous ligand for the growth
RT      hormone secretagogue receptor.";
RL      Trends Endocrinol. Metab. 12:118-122(2001).
CC      -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC      receptor type 1 (GHSR) inducing the release of growth hormone from
CC      the pituitary. Has an appetite-stimulating effect, induces
CC      adiposity and stimulates gastric acid secretion. Involved in
CC      growth regulation.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1; Synonyms=Ghrelin;
CC      IsoId=Q9QYH7-1; Sequence=Displayed;
CC      Name=2; Synonyms=del-Gln14-ghrelin;
CC      IsoId=Q9QYH7-2; Sequence=VSP_003248;
CC      -!- TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC      the stomach. Very low levels are detected in the hypothalamus,
CC      heart, lung, pancreas, intestine and adipose tissue.
CC      -!- PTM: O-n-octanoylation is essential for activity. The replacement
CC      of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC      -!- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC      RANGE=24-51 (Q9QYH7-1); NOTE=Ref.1.
CC      -!- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC      RANGE=24-50 (Q9QYH7-2); NOTE=Ref.2.
CC      -!- SIMILARITY: Belongs to the motilin family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AB029433; BAA89370.1; -; mRNA.
CC      EMBL; AB035699; BAB11956.1; -; mRNA.
CC      PIR; B59316; B59316.
CC      Ensembl; ENSRNOG0000010349; Rattus norvegicus.
CC      RGD; 632283; Ghrl.
CC      GO; GO:0005615; Extracellular space; IC.
CC      GO; GO:001664; F:G-protein-coupled receptor binding; IPI.
CC      GO; GO:0016608; F:growth hormone-releasing hormone activity; IDA.
CC      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IDA.
CC      GO; GO:0050791; P:regulation of physiological process; NAS.
```

DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Alternative splicing; Direct protein sequencing; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 Ghrelin.
 FT PEPTIDE 24 51 Removed in mature form.
 FT PROPEP 52 117 O-octanoyl serine.
 FT LIPID 26 26 Missing (in isoform 2).
 FT VARSPPLIC 37 37 /FTID=VSP_003248.
 SQ SEQUENCE 117 AA; 13176 MW; 8957546FE51A7691 CRC64;
 Query Match 84.8%; Score 518; DB 1; Length 117;
 Best Local Similarity 82.9%; Pred. No. 3.6e-44;
 Matches 97; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MPSFGTVCSSLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 DB 1 MVSSATICSLLLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 QY 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQHQSOALGKFLQDILWEEAKEAPADK 117
 DB 61 DRGQAEAELEIRFNAPFDVGIKLSGAQYQHQGRALGKFLQDILWEEVKEATDK 117
 RESULT 5
 ID Q8CH53 MERUN PRELIMINARY; PRT; 117 AA.
 AC Q8CH53;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ghrelin preproprotein.
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Gerbillinae; Meriones.
 OC NCBI_TaxID=10047;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14724148; DOI=10.1136/gut.2003.021568;
 RA Suzuki H., Masaoka T., Hosoda H., Ota T., Minegishi Y., Nomura S.,
 RT "Helicobacter pylori infection modifies gastric and plasma ghrelin
 dynamics in Mongolian gerbils.";
 RL Gut 53:187-194(2004).
 DR EMBL; AF442491; AAC06965.1; -; mRNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0016608; P:regulation of hormone-releasing hormone activity; IEA.
 DR GO; GO:0050791; P:regulation of physiological process; IEA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
 Query Match 84.3%; Score 515; DB 2; Length 117;
 Best Local Similarity 82.1%; Pred. No. 7.2e-44;
 Matches 96; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MPSFGTVCSSLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 DB 1 MMSSGTICSSLLGLVLMVDMVAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPD 60

QY 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQHQSOALGKFLQDILWEEAKEAPADK 117
 DB 61 GRGQAEAGAELEIRFNAPFDVGIKLSGAQYQHQGRALGKFLQDILWEEVKEATDK 117
 RESULT 6
 ID GHRL FELCA STANDARD; PRT; 117 AA.
 AC Q6BEG6; Q6BEG5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 releasing peptide) (Motilin-related peptide).
 GN Name=GHRL;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 OC NCBI_TaxID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC TISSUE=Stomach;
 RA Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
 RT "cDNA cloning of feline and caprine ghrelin.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 receptor type 1 (GHSR) inducing the release of growth hormone from
 the pituitary. Has an appetite-stimulating effect, induces
 adiposity and stimulates gastric acid secretion. Involved in
 growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q6BEG6-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q6BEG6-2; Sequence=VSP_011626;
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: Belongs to the motilin family.
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 use as long as its content is in no way modified and this statement is not
 removed.
 DR EMBL; AB089201; BAD34670.1; -; mRNA.
 DR EMBL; AB089202; BAD34671.1; -; mRNA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Alternative splicing; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 51 Ghrelin (By similarity).
 FT PROPEP 52 117 Removed in mature form (By similarity).
 FT LIPID 26 26 O-octanoyl serine (By similarity).
 FT VARSPPLIC 37 37 Missing (in isoform 2).
 FT /FTID=VSP_011626.
 SQ SEQUENCE 117 AA; 12956 MW; 8235A51447FF530 CRC64;
 Query Match 83.6%; Score 511; DB 1; Length 117;
 Best Local Similarity 82.9%; Pred. No. 1.8e-43;
 Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MPSFGTVCSSLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 DB 1 MMSSGTICSSLLGLVLMVDMVAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPD 60

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Db 1 MPSPTVCSLLLFMSLWADLAMAGSSFLSPHOKVQORKEKPKPAKLQPRALEGLIHP6 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DTSQVEGADELEIRFNAPFDVGIKLSGAQYHQHQAQHGKFLQDVLWEEADEVLAD6 117

RESULT 7
GHR_L_CANFA
ID GHR_L_CANFA STANDARD; PRT; 117 AA.
AC Q9BEF8; Q9BEF7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
GN Name=GHR_L; Synonyms=MTLRP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
RC TISSUE=Stomach; fundus;
RA Tonasetto C., Wendling C., Rio M.-C., Poitras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC TISSUE=Stomach;
RA Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
RT "Dog ghrelin."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces in
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9BEF8-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9BEF8-2; Sequence=VSP 003244;
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: Belongs to the motilin family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; AJ298295; CAC29155.1; -; mRNA.
DR EMBL; AJ298296; CAC29156.1; -; mRNA.
DR EMBL; AB060700; BAC75928.1; -; mRNA.
DR Ensembl; ENSCAFG0000005129; Canis familiaris.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Alternative splicing; Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23 By similarity.
FT PEPTIDE 24 51 Ghrelin (By similarity).
FT PROPEP 52 117 Removed in mature form (By similarity).
FT LIPID 26 26 O-octanoyl serine (By similarity).
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FT VARSPLIC 37 37 Missing (in isoform 2).
FT SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;
SQ Query Match 77.9%; Score 476; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 6.1e-40;
Matches 91; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLFMSLWADLAMAGSSFLSPHOKVQORKEKPKPAKLQPRALAGWL60
Db 1 MPSLGTMCSSLLLFMSLWADLAMAGSSFLSPHOKVQORKEKPKPAKLQPRALAGSL60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DTSQVEGADELEIRFNAPFDVGIKLSGAQYHQHQAQHGKFLQDVLWEEADEVLAD6 117

RESULT 8
GHR_L_PIG
ID GHR_L_PIG STANDARD; PRT; 118 AA.
AC Q9GKY5; Q9BDG8; Q9GKY4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
GN Name=GHR_L;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
RA Kojima M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
RC TISSUE=Stomach;
RA Roussellet J., Lacroix D., Dubreuil P.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces in
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9GKY5-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9GKY5-2; Sequence=VSP 003247;
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: Belongs to the motilin family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; AB035703; BAB19048.1; -; mRNA.
DR EMBL; AB035704; BAB19049.1; -; mRNA.
DR EMBL; AF308930; AAK19243.1; -; mRNA.
DR EMBL; AY028942; AAK30002.1; -; mRNA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.

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DR ProDom; PD332162; Preproghrelin; 1.
 KW SIGNAL 1 24 By similarity; Hormone; Lipoprotein; Signal.
 FT PEPTIDE 25 52 Ghrelin.
 FT PROPEP 53 118 Removed in mature form (By similarity).
 FT LIPID 27 27 O-octanoyl serine (By similarity).
 FT VARSPLIC 38 38 Missing (in isoform 2).
 FT CONFLICT 17 17 /FTID=VSP_003247.
 FT CONFLICT 72 72 L -> P (in Ref. 2; AAK30002).
 FT CONFLICT 72 72 K -> E (in Ref. 2; AAK30002).
 SQ SEQUENCE 118 AA; 12786 MW; 856D3E1D6DABIA76 CRC64;

Query Match 77.3%; Score 472.5; DB 1; Length 118;
 Best Local Similarity 78.0%; Pred. No. 1.4e-39;
 Matches 92; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 1 MPSPTGVCSSLLLLGMLWLDLWAGSSFLSPHQRVQQRKSKPPAKLPQPRALAGWLRP 59
 DB 1 MPSTGTICSLLLSVLLMADLAMAGSSFLSPHQVQQRKSKPPAKLPQPRALAGWLCP 60
 QY 60 EDGQAGAEDELEVRFNAPFDVGIKLGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 EDSGEVEGTKEIRFNAPCDVGIKLGSAGSDHQGPLGKFLQDILWEEVTEAPADK 118

RESULT 9
 GHRL_CAPHI STANDARD; PRT; 116 AA.
 ID Q6BEG7;
 AC Q6BEG7;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
 GN Name=GHRL;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Stomach;
 RA Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
 RT "cDNA cloning of feline and caprine ghrelin.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.

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 CC -----
 CC EMBL; AB089200; BAD34669.1; -; mRNA.
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC PANTHER; PTHR14122; Preproghrelin; 1.
 CC Pfam; PF04643; Motilin_assoc; 1.
 CC Pfam; PF04644; Motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD332162; Preproghrelin; 1.
 CC Hormone; Lipoprotein; Signal.
 KW SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 50 Ghrelin (By similarity).
 FT

FT PROPEP 51 116 Removed in mature form (By similarity).
 FT LIPID 26 26 O-octanoyl serine (By similarity).
 SQ SEQUENCE 116 AA; 12935 MW; CDA67971D72E3303 CRC64;

Query Match 71.4%; Score 436.5; DB 1; Length 116;
 Best Local Similarity 71.8%; Pred. No. 5.7e-36;
 Matches 84; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 1 MPSPTGVCSSLLLLGMLWLDLWAGSSFLSPHQRVQQRKSKPPAKLPQPRALAGWLRP 60
 DB 1 MPARTTICSLLLSLLMWMDLWAGSSFLSPHQKL-QRKEPKKSGRLKPRALEGQFDDP 59
 QY 61 DGGQAGAEDELEVRFNAPFDVGIKLGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 60 VGSQEGAEDELEIRFNAPFNIGIKLSAQSLQHGQTLGKFLQDILWEEAETLADE 116

RESULT 10
 Q863LO SHEEP PRELIMINARY; PRT; 116 AA.
 ID Q863LO;
 AC Q863LO;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Preproghrelin precursor.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach;
 RA Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
 RT "sheep ghrelin.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB060599; BAC75928.1; -; mRNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
 DR GO; GO:0050791; P:regulation of physiological process; IEA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Signal.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 50 ghrelin.
 SQ SEQUENCE 116 AA; 12977 MW; B78ECA3DBF0E568E CRC64;

Query Match 59.1%; Score 422.5; DB 2; Length 116;
 Best Local Similarity 70.1%; Pred. No. 1.5e-34;
 Matches 82; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 1 MPSPTGVCSSLLLLGMLWLDLWAGSSFLSPHQRVQQRKSKPPAKLPQPRALAGWLRP 60
 DB 1 MPARTTYSLLLSLLMWMDLWAGSSFLSPHQKL-QRKEPKKSGRLKPRALEGQFDDP 59
 QY 61 DGGQAGAEDELEVRFNAPFDVGIKLGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 60 VGSQEGAEDELEIRFNAPFNIGIKLSAQSLQHGQTLGKFLQDILWEEAETLADE 116

RESULT 11
 GHRL_BOVIN STANDARD; PRT; 116 AA.
 ID Q9BDJ6; Q9GKV6;
 AC Q9BDJ6; Q9GKV6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:24:12 ; Search time 220.509 Seconds
(without alignments)
1171.032 Million cell updates/sec

Title: US-09-718-803A-5
Perfect score: 1905
Sequence: 1 MNWNPSEEPGNLTADLD.....KLSTLKDESSRAWTESSINT 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1905	100.0	366	1	GHSR HUMAN	Q2847 homo sapien
2	1855	97.4	360	2	Q6B7N9_MACFA	Q6b7n9 macaca fasc
3	1789	93.9	364	1	GHSR RAT	Q08725 rattus norv
4	1788	93.9	364	1	GHSR MOUSE	Q99p50 mus musculu
5	1771	93.0	366	1	GHSR_PIG	Q95254 sus scrofa
6	1754	92.1	366	2	Q8MH75_SHEEP	Q8mh75 ovis aries
7	1411	74.1	347	2	Q7ZT14_CHICK	Q7zt14 gallus gall
8	1388	72.9	289	2	Q6ISR8_HUMAN	Q6isr8 homo sapien
9	1308	68.7	331	2	Q7ZZJ9_CHICK	Q7zzj9 gallus gall
10	1105	58.0	385	2	Q6YQ23_ACASC	Q6yq23 acanthopagr
11	1079.5	56.7	374	2	Q93412_PPERC	Q93412 spherooides
12	1075.5	56.5	394	2	Q4STY3_TETNG	Q4sty3 tetraodon n
13	1010	53.0	267	2	Q7ZZJ8_CHICK	Q7zzj8 gallus gall
14	871	45.7	215	2	Q711Q7_CHICK	Q711q7 gallus gall
15	863.5	45.3	412	1	MTLR_HUMAN	Q43193 homo sapien
16	862	45.2	363	2	Q93413_PPERC	Q93413 spherooides
17	832.5	43.7	211	2	Q711Q8_CHICK	Q711q8 gallus gall
18	809.5	42.5	295	2	Q6YQ22_ACASC	Q6yq22 acanthopagr
19	792	41.6	286	2	Q4RFP2_TETNG	Q4rfp2 tetraodon n
20	696	36.5	145	2	Q97914_SHEEP	Q97914 ovis aries
21	648.5	34.0	514	2	Q4SB84_TETNG	Q4sb84 tetraodon n
22	648	34.0	559	2	Q93414_PPERC	Q93414 spherooides
23	620	32.5	123	2	Q80UB2_MOUSE	Q80ub2 mus musculu
24	569.5	29.9	117	2	Q58M10_RAT	Q58m10 rattus norv
25	494.5	26.0	327	2	Q4S774_TETNG	Q4s774 tetraodon n
26	483.5	25.4	424	1	NTRI1_MOUSE	Q08319 mus musculu
27	481.5	25.3	365	2	Q4SP89_TETNG	Q4sp89 tetraodon n
28	478	25.1	407	2	Q58CW4_BOVIN	Q58cw4 bos taurus
29	475.5	25.0	413	2	Q65Y84_BOMMO	Q65y84 bombyx mori
30	471	24.7	493	2	Q7RTK4_ANOGA	Q7rtk4 anopheles g
31	468.5	24.6	395	2	Q8BZ39_MOUSE	Q8bz39 mus musculu

RESULT 1

GHSR HUMAN

ID _GHSR_HUMAN STANDARD; PRT; 366 AA.

AC Q92847; Q92848; Q96RJ7;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing

peptide receptor) (GHRP) (Ghrelin receptor).

DE Name=GHSR;

GN Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1A AND 1B).

RC TISSUE=Pituitary;

RX MEDLINE=96337998; PubMed=8688086;

RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberato P.A.,

RA Rosenblum C.I., Hamelin M., Hreniuk D.L., Palyha O.C., Anderson J.,

RA Pareess P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S.,

RA Chaung L.-Y., Elbrecht A., Dashkevich M., Heavens R., Rigby M.,

RA Sirinathsinghji D.J.S., Dean D.C., Melillo D.G., Patchett A.A.,

RA Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M.,

RA Smith R.G., van der Ploeg L.H.T.;

RT "A receptor in pituitary and hypothalamus that functions in growth

hormone release.";

RL Science 273:974-977(1996).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1A AND 1B).

RX MEDLINE=21255649; PubMed=11356716; DOI=10.1210/en.142.6.2649;

RA Petersenn S., Rasch A.C., Penschorn M., Beil F.U., Schulte H.M.;

RA "Genomic structure and transcriptional regulation of the human growth

hormone secretagogue receptor.";

RL Endocrinology 142:2649-2659(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1A AND 1B).

RA Kopatz S.A., Aronstam R.S., Sharma S.V.;

RT "cDNA clones of human proteins involved in signal transduction

sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [4]

RP FUNCTION.

RX MEDLINE=21219832; PubMed=11322507; DOI=10.1385/ENDO.14.1.009;

RA Smith R.G., Leonard K.R., Bailey A.R.T., Palyha O.C., Feighner S.D.,

RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;

RT "Growth hormone secretagogue receptor family members and ligands.";

RL Endocrine 14:9-14(2001).

RN [5]

RP FUNCTION.

RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;

RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;

RT "Ghrelin is a growth-hormone-releasing acylated peptide from

32 468 24.6 422 2 Q538H7_RANCA
33 466.5 24.5 395 2 Q91276_MOUSE
34 464 24.4 418 1 NTRI1_HUMAN
35 463.5 24.3 395 2 Q9ESQ4_RAT
36 463.5 24.3 395 2 Q9JIB1_RAT
37 461.5 24.2 424 1 NTRI1_RAT
38 461.5 24.2 556 1 CAPAR_DROME
39 459 24.1 346 2 Q5ICC7_HELAM
40 458 24.0 346 2 Q6VYH4_HELZE
41 454.5 23.9 426 2 Q8NE20_HUMAN
42 452.5 23.8 403 2 Q7LDP6_HUMAN
43 452.5 23.8 426 2 Q9HB89_HUMAN
44 445 23.4 415 2 Q96AMS_HUMAN
45 444 23.3 412 2 Q7LCS4_HUMAN

ALIGNMENTS

```

RT  stomach. ";
RL  Nature 402:656-660(1999).
CC  -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC  Stimulates growth hormone secretion. Binds also other growth
CC  hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC  as well as non-peptide, low molecular weight secretagogues (e.g.
CC  L-692,429, MK-0677, adenosine).
CC  L-692,429, MK-0677, adenosine).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=1A;
CC  IsoId=Q92847-1; Sequence=Displayed;
CC  Name=1B;
CC  IsoId=Q92847-2; Sequence=VSP_001916, VSP_001917;
CC  TISSUE SPECIFICITY: Pituitary and hypothalamus.
CC  -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; U60179; AAC50653.1; -; mRNA.
DR  EMBL; U60181; AAC50654.1; -; mRNA.
DR  EMBL; AF369786; AAK71539.1; -; Genomic DNA.
DR  EMBL; AF369786; AAK71540.1; -; Genomic DNA.
DR  EMBL; AY429112; AAR07907.1; -; mRNA.
DR  EMBL; AY322544; AAP84357.1; -; Genomic DNA.
DR  Ensembl; ENSG00000121853; Homo sapiens.
DR  HGNC; HGNC:4267; GHSR.
DR  MIM; 601898; -.
DR  GO; GO:0016021; C:integral to membrane; TAS.
DR  GO; GO:0005886; C:plasma membrane; TAS.
DR  GO; GO:0004930; P:G-protein coupled receptor activity; TAS.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR  InterPro; IPR003905; GHS1_receptor.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  PANTHER; PTHR19284:SP51; GHS1_receptor; 1.
DR  Pfam; PF00001; 7tm.1; 1.
DR  PRINTS; PR01417; GHSRECEPTOR.
DR  PRINTS; PR00237; GPCR_RHODOPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW  Receptor; Transducer; Transmembrane.
FT  TOPO_DOM 1 40 Extracellular (Potential).
FT  TRANSMEM 41 66 1 (Potential).
FT  TOPO_DOM 67 72 Cytoplasmic (Potential).
FT  TRANSMEM 73 96 2 (Potential).
FT  TOPO_DOM 97 117 Extracellular (Potential).
FT  TRANSMEM 118 139 3 (Potential).
FT  TOPO_DOM 140 162 Cytoplasmic (Potential).
FT  TRANSMEM 163 183 4 (Potential).
FT  TOPO_DOM 184 211 Extracellular (Potential).
FT  TRANSMEM 212 235 5 (Potential).
FT  TOPO_DOM 236 263 Cytoplasmic (Potential).
FT  TRANSMEM 264 285 6 (Potential).
FT  TOPO_DOM 286 302 Extracellular (Potential).
FT  TRANSMEM 303 326 7 (Potential).
FT  TOPO_DOM 327 366 Cytoplasmic (Potential).
FT  CARBOHYD 13 13 N-linked (GlcNAc. . .) (Potential).
FT  CARBOHYD 27 27 N-linked (GlcNAc. . .) (Potential).
FT  DISULFID 116 198 By similarity.
FT  VARSPPLIC 266 289 AVVVFALICMLPFHVGRIYFSKS -> GGSQRALRLSLAG
FT  PLSLCLPLSL (in isoform 1B).
FT  FTId=VSP_001916.
FT  VARSPLIC 290 366 Missing (in isoform 1B).
FT  FTId=VSP_001917.
FT  VARSPLIC 366 AA; 41329 MW; D1B62710DA9DC0C6 CRC64;
SQ  SEQUENCE 366 AA; 41329 MW; D1B62710DA9DC0C6 CRC64;
Query Match 100.0%; Score 1905; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 366; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWNATPSEPGFNLTADLDWDASPGNDLSGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
DB 1 MWNATPSEPGFNLTADLDWDASPGNDLSGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
QY 61 NLLTMLVVSRRFRLRTTNLYLSSMAFSDLLIFLCMPDLVLRLWQYRPNWFGDLLCKLFQ 120
DB 61 NLLTMLVVSRRFRLRTTNLYLSSMAFSDLLIFLCMPDLVLRLWQYRPNWFGDLLCKLFQ 120
QY 121 FVSECTVATVLTITALSVERYFAICFPLRAKVVTWGRVKLVFVIWAVAFCSAGPIFV 180
DB 121 FVSECTVATVLTITALSVERYFAICFPLRAKVVTWGRVKLVFVIWAVAFCSAGPIFV 180
QY 191 LVGVEHENGTPDWTNECRPTPEFAVRSGLLITVMWSSIFFPFLPVFCLTIVLSLGRKLW 240
DB 191 LVGVEHENGTPDWTNECRPTPEFAVRSGLLITVMWSSIFFPFLPVFCLTIVLSLGRKLW 240
QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSPFGSLIAQI 300
DB 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSPFGSLIAQI 300
QY 301 SQYCNLVSVFLYLSAAINPILYNIMSKYRVAVFRLIGFEPFQSQRKSLTLKDESSRAWT 360
DB 301 SQYCNLVSVFLYLSAAINPILYNIMSKYRVAVFRLIGFEPFQSQRKSLTLKDESSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366
RESULT 2
Q6B7N9 MACFA PRELIMINARY; PRT; 360 AA.
AC Q6B7N9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Growth hormone secretagogue receptor (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hellings S.E. III.;
RL "Macaca fascicularis growth hormone secretagogue receptor cloning.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AY675630; AAT77421.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 360 AA; 40700 MW; DAC4AC726EE9468E CRC64;
Query Match 97.4%; Score 1855; DB 2; Length 360;
Best Local Similarity 98.9%; Pred. No. 4.3e-122;
Matches 356; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 7 SEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIGIAGNLTML 66
 Db 1 SEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIGIAGNLTML 60
 QY 67 VVSFRFRLTNTNLYLSSMAFSDLLIFLCMPDLVRLWQVPMFNGDGLLCKLFOFVSESC 126
 Db 61 VVSFRFRLTNTNLYLSSMAFSDLLIFLCMPDLVRLWQVPMFNGDGLLCKLFOFVSESC 120
 QY 127 TYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFVVLVGVGH 186
 Db 121 TYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFVVLVGVGH 180
 QY 187 ENGTPDWDNTECRTEFAVRSGLLTVMVWSSIFFFLPVCLTVLYSLIGRKLWRRRGD 246
 Db 181 ENGTPDWDNTECRTEFAVRSGLLTVMVWSSIFFFLPVCLTVLYSLIGRKLWRRRGD 240
 QY 247 AVVGASLRDQNHQKTVKMLAVVFAFVILCMPLDVLVRLWQVPMFNGDGLLCKLFOFVSESC 306
 Db 241 AVVGASLRDQNHQKTVKMLAVVFAFVILCMPLDVLVRLWQVPMFNGDGLLCKLFOFVSESC 300
 QY 307 VSFVLFYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQRSKSLTKDESSRAWTESSINT 366
 Db 301 VSFVLFYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQRSKSLTKDESSRAWTESSINT 360

RESULT 3
 GHSR_RAT STANDARD; PRT; 364 AA.
 AC 008725;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
 peptide receptor) (GHRP) (Ghrelin receptor).
 GN Name=Ghr;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pituitary;
 RX MEDLINE=97246555; PubMed=9092793; DOI=10.1210/me.11.4.415;
 RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P.,
 RA Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;
 RT "Molecular analysis of rat pituitary and hypothalamic growth hormone
 secretagogue receptors.";
 RL Mol. Endocrinol. 11:415-423(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 1-240.
 RC STRAIN=Wistar; TISSUE=Pituitary;
 RX MEDLINE=98100386; PubMed=9437732; DOI=10.1016/S0196-9781(97)00263-5;
 RA Yokote R., Sato M., Matsubara S., Onye H., Nimi M., Murao K.,
 RA Takahara J.;
 RT "Molecular cloning and gene expression of growth hormone-releasing
 peptide receptor in rat tissues.";
 RL Peptides 19:15-20(1998).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 stomach.";
 RL Nature 402:656-660(1999).
 CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
 CC Stimulates growth hormone secretion. Binds also other growth
 CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
 CC as well as non-peptide, low molecular weight secretagogues (e.g.
 CC L-692,429, MK-0677, adenosine) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U94321; AAC53156.1; -; mRNA.
 DR EMBL; AB001982; BAA21777.1; ALT INIT; mRNA.
 DR Ensembl; ENSRNOG0000024119; Rattus norvegicus.
 DR RGD; 621397; Ghr.
 DR GO; GO:0016021; C: integral to membrane; TAS.
 DR GO; GO:0005331; F: growth hormone receptor binding; TAS.
 DR GO; GO:0001616; F: growth hormone secretagogue receptor activity; IDA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IDA.
 DR GO; GO:0045923; P: positive regulation of fatty acid metabolism; IMP.
 DR InterPro; IPR003905; GHS1_receptor.
 DR InterPro; IPR000276; GPCR_Rhodops.
 DR PANTHER; PTHR19264.SF51; GHS1_receptor; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01417; GHSRECEPTOR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 KW Transmembrane.
 CC FT TOPO_DOM 1 40 Extracellular (Potential).
 CC FT TRANSMEM 41 66 1 (Potential).
 CC FT TOPO_DOM 67 72 Cytoplasmic (Potential).
 CC FT TRANSMEM 73 96 2 (Potential).
 CC FT TOPO_DOM 97 117 Extracellular (Potential).
 CC FT TRANSMEM 118 139 3 (Potential).
 CC FT TOPO_DOM 140 162 Cytoplasmic (Potential).
 CC FT TRANSMEM 163 183 4 (Potential).
 CC FT TOPO_DOM 184 211 Extracellular (Potential).
 CC FT TRANSMEM 212 235 5 (Potential).
 CC FT TOPO_DOM 236 285 Cytoplasmic (Potential).
 CC FT TRANSMEM 286 302 Extracellular (Potential).
 CC FT TOPO_DOM 303 326 7 (Potential).
 CC FT TRANSMEM 327 364 Cytoplasmic (Potential).
 CC FT CARBOHYD 13 13 N-linked (GlcNAc. .) (Potential).
 CC FT CARBOHYD 26 26 N-linked (GlcNAc. .) (Potential).
 CC FT CARBOHYD 187 187 N-linked (GlcNAc. .) (Potential).
 CC FT DISULFID 115 197 By similarity.
 CC SQ SEQUENCE 364 AA; 40963 MW; DCBF559BE061EE9 CRC64;
 Query Match 93.9%; Score 1789; DB 1; Length 364;
 Best Local Similarity 95.6%; Pred. No. 1.8e-117; Indels 2; Gaps 2;
 Matches 350; Conservative 5; Mismatches 9;
 QY 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIGIAG 60
 Db 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIGIAG 59
 QY 61 NLTLMLVVSFRFRLTNTNLYLSSMAFSDLLIFLCMPDLVRLWQVPMFNGDGLLCKLFO 120
 Db 60 NLTLMLVVSFRFRLTNTNLYLSSMAFSDLLIFLCMPDLVRLWQVPMFNGDGLLCKLFO 119
 QY 121 FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFV 180
 Db 120 FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFV 179
 QY 181 LVGVEHENGTPDWDNTECRTEFAVRSGLLTVMVWSSIFFFLPVCLTVLYSLIGRKLW 240
 Db 180 LVGVEHENGTPDWDNTECRTEFAVRSGLLTVMVWSSIFFFLPVCLTVLYSLIGRKLW 239
 QY 241 RRRRGDAVVGASLRDQNHQKTVKMLAVVFAFVILCMPLDVLVRLWQVPMFNGDGLLCKL 300
 Db 240 -RRRGDAVVGASLRDQNHQKTVKMLAVVFAFVILCMPLDVLVRLWQVPMFNGDGLLCKL 298
 QY 301 SQYCNLVSVFLVYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQRSKSLTKDESSRAW 360
 Db 299 SQYCNLVSVFLVYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQRSKSLTKDESSRAW 358

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QY 361 ESSINT 366
Db 359 KSSINT 364

RESULT 4
GHSR_MOUSE
ID GHSR_MOUSE STANDARD; PRT; 364 AA.
AC Q99P50; QBWXX9; Q91282;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghsr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Fothergill A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gusincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenawa Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Yasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 1-183
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA Kacsoh B.;
RT "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by
RT rapid amplification of cDNA ends (RACE).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 73-257.
RC STRAIN=129S3/SvimJ;
RA Peng X., Frohman L.A., Kineman R.D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AK049671; BACJ3866.1; -; mRNA.
CC EMBL; AY056474; AALJ3336.1; -; mRNA.
CC EMBL; AF332997; AAG61141.1; -; mRNA.
CC Ensembl; ENSMUSG0000051136; Mus musculus.
CC MGI; MGI:2441906; Ghsr.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0001616; F:growth hormone secretagogue receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC PANTHER; PTHR19264:SF51; GHS1_receptor; 1.
CC Pfam; PF00001; 7tm.1. 1.
CC PRINTS; PR01417; GHSRECEPTOR.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
CC KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
CC Transmembrane.
FT TOPO_DOM 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT TOPO_DOM 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).
FT TOPO_DOM 97 117 Extracellular (Potential).
FT TRANSMEM 118 139 3 (Potential).
FT TOPO_DOM 140 162 Cytoplasmic (Potential).
FT TRANSMEM 163 183 4 (Potential).
FT TOPO_DOM 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT TOPO_DOM 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT TOPO_DOM 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT TOPO_DOM 327 364 Cytoplasmic (Potential).
FT CARBOHYD 13 13 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 187 187 N-linked (GlcNAc. .) (Potential).
FT DISULFID 115 197 By similarity.
FT CONFLICT 59 59 G -> S (in Ref. 2).
SQ SEQUENCE 364 AA; 40969 MW; 8F1214E58EF3B2E8 CRC64;
Query Match 93.9%; Score 1788; DB 1; Length 364;
Best Local Similarity 95.4%; Pred. No. 2.2e-117;
Matches 349; Conservative 6; Mismatches 9; Indels 2; Gaps 2;
QY 1 MNATPSEEPGNITLADLDWDASFGNDSLGDELLQLPAPPLAGVTATCVAFVVGATG 60
Db 1 MNATPSEEPGNVTL-DLDWDASFGNDSLGDELLPLPAPPLAGVTATCVAFVVGISG 59
QY 61 NLLTMLVVSREFRLTTNLYLSSWAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Db 60 NLLTMLVVSREFRLTTNLYLSSWAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 119
QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVFVIVAWAFCSAGPIFV 180
Db 120 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVVIVAWAFCSAGPIFV 179
QY 181 LVGVEHNGTDPWDTNECRPTFAVRSGLLITVMWVSSIIFPFLPVFCLTVLYSLIGRLW 240
Db 180 LVGVEHNGTDPWDTNECRPTFAVRSGLLITVMWVSSIIFPFLPVFCLTVLYSLIGRLW 239
QY 241 RRRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPFHVGRVLFKSPFPGSLIAQI 300
Db 240 -RRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPFHVGRVLFKSPFPGSLIAQI 298
QY 301 SQYCNLYSVLIFYLSAAINPILYIMSKKYRVAVFRLGFPFPGSQRLSTLKDESSRAWT 360
Db 301 SQYCNLYSVLIFYLSAAINPILYIMSKKYRVAVFRLGFPFPGSQRLSTLKDESSRAWT 360

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Db 299 SOYCNLVSVFVLYLSAAINPILYNIMSKYRVAVFKLLGFBSFSQKSLSTLKDESSRAWT 358
Qy 361 ESSINT 366
Db 359 KSSINT 364

RESULT 5
ID GHRS_PIG STANDARD; PRT; 366 AA.
AC Q95254; Q95255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=GHSR;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1A AND 1B).
RC STRAIN=Yorkshire; TISSUE=Pituitary;
RX MEDLINE=96337998; PubMed=8688086;
RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberato P.A.,
RA Rosenblum C.I., Hamelin M., Hreniuk D.L., Palaya O.C., Anderson J.,
RA Pares P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S.,
RA Chang L.-Y., Elbrecht A., Dashkevich M., Heavens R., Rigby M.,
RA Srinathalingji D.J.S., Dean D.C., Melillo D.G., Patchett A.A.,
RA Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M.,
RA Smith R.G., van der Ploeg L.H.T.;
RT "A receptor in pituitary and hypothalamus that functions in growth
hormone release".
RL Science 273:974-977 (1996).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692, 429, MK-0677, adenosine).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1A;
CC IsoId=Q95254-1; Sequence=Displayed;
CC Name=1B;
CC IsoId=Q95254-2; Sequence=VSP_001918, VSP_001919;
CC -!- TISSUE SPECIFICITY: Pituitary and hypothalamus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U60178; AAC48630.1; -; mRNA.
CC EMBL; U60180; AAC48631.1; -; mRNA.
CC InterPro; IPR003905; GHS1_receptor.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC PANTHER; PTHR19264:SF51; GHS1_receptor; 1.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR01417; GHSRECEPTOR.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
CC Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT TOPO_DOM 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).

FT TOPO_DOM 97 117 Extracellular (Potential).
FT TRANSMEM 118 139 3 (Potential).
FT TOPO_DOM 140 162 Cytoplasmic (Potential).
FT TRANSMEM 163 183 4 (Potential).
FT TOPO_DOM 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT TOPO_DOM 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT TOPO_DOM 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT TOPO_DOM 327 366 Cytoplasmic (Potential).
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).
FT DISULFID 116 198 By similarity.
FT VARSPPLIC 266 289 AVVVFATILCWLPHPVGRYLFPSKS -> GGSQCALELSLPG
FT PLHSSCLFSSP (in isoform 1B).
FT /FTID=VSP_001918.
FT /Missing (in isoform 1B).
FT /FTID=VSP_001919.
SQ SEQUENCE 366 AA; 41195 MW; 2C850B3EF61B7C1C CRC64;
Query Match 93.08; Score 1771; DB 1; Length 366;
Best Local Similarity 93.2%; Pred. No. 3.4e-116;
Matches 341; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGIA 60
Db 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGIA 60
Qy 61 NLITMLVSVRFRELTNTNLYLSMAFSDLLIFLCMPDLVRLVQYRPNWPGDILCKLFQ 120
Db 61 NLITMLVSVRFRELTNTNLYLSMAFSDLLIFLCMPDLVRLVQYRPNWPGDILCKLFQ 120
Qy 121 FVSESCYATVLTITALSVERVFAICPLRAKVVVTKGRVKLVFVWAVAFCSAGPIFV 180
Db 121 FVSESCYATVLTITALSVERVFAICPLRAKVVVTKGRVKLVFVWAVAFCSAGPIFV 180
Qy 181 LVGVHEHNGTDPMDTNECRTEPAVRSGLLTVMWVSSIFFFLPVFCITLVLYSLIGRKLW 240
Db 181 LVGVHEHNGTDPMDTNECRTEPAVRSGLLTVMWVSSIFFFLPVFCITLVLYSLIGRKLW 240
Qy 241 RRRRGDAVGCASLRDQNHKOTVMKLA VVFAFICWLPFHVGRYLFPSKSPGSLIAQI 300
Db 241 RRRRGDAVGCASLRDQNHKOTVMKLA VVFAFICWLPFHVGRYLFPSKSPGSLIAQI 300
Qy 301 SOYCNLVSVFVLYLSAAINPILYNIMSKYRVAVFKLLGFBSFSQKSLSTLKDESSRAWT 360
Db 301 SOYCNLVSVFVLYLSAAINPILYNIMSKYRVAVFKLLGFBSFSQKSLSTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366

RESULT 6
Q8MHZ5_SHEEP
ID Q8MHZ5_SHEEP PRELIMINARY; PRT; 366 AA.
AC Q8MHZ5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Ghrelin/growth hormone secretagogue receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary gland;
RA Murata T., Ikegami R., Morita Y., Shinozaki K.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; AY093949; AAM19734.1; -; mRNA.
 DR EMBL; AY093950; AAM19735.1; -; mRNA.
 DR EMBL; AY093948; AAM19733.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003905; GHS1_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01417; GHSRECEPTOR.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 366 AA; 41487 MW; 2F276651BC6CSD57 CRC64;

Query Match 92.1%; Score 1754; DB 2; Length 366;
 Best Local Similarity 92.3%; Pred. No. 5.2e-115;
 Matches 338; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 MNATPSEPGFNLTADLDWDASPGNDLGLDELQLPAPLAGVATCTVALFVVGIA 60
 DB 1 MNATRSEELGNLTLPDLDDAAFDNDLSLTDLPPLPAPLAGVATCTVALFVVGIA 60

QY 61 NLLTMLVVSRRFELRTTNLNLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
 DB 61 NLLTMLVVSRRFELRTTNLNLSSMAFSDLLIFLCMPDLVRLWYRPNWFGDLLCKLFQ 120

QY 121 FVSECTVATVLTITALSVERFAICFPLRAKVVTGKRVKLVIVIVAVAFCSAGPIFV 180
 DB 121 FVSECTVATVLTITALSVERFAICFPLRAKVVTGKRVKLVIAIWAFAFCSAWPIFM 180

QY 181 LVGVEHENGTPDNECRPTFAVRSGLLTVMWVSSIFFPVFCITVLYSLIGRKLW 240
 DB 181 LVGVEHENGTPDNECRATEFAVRSGLLTVMWVSSIFFPVFCITVLYSLIGRKLW 240

QY 241 RRRRGDAVVGASLRDQNHQKQTVKMLAVVVFAPILCWLPHFVGRYLFKSFPGSLEIAQI 300
 DB 241 RRRSEVVVGASLRDQNHQKQTVKMLAVVVFAPVLCWLPHFVGRYLFKSFPGSVEIAQI 300

QY 301 SQYCNLVSEVLYFYLGAANPILYNIMSKKYRVAVFRLGFPFSPQRKSLTKDESSRAWT 360
 DB 301 SQYCNLVSEVLYFYSAAINPILYNIMSKKYRVAVFRLGFPFSPQRKSLTKDESSRAWT 360

QY 361 ESSINT 366
 DB 361 ESSINT 366

RESULT 7
 Q7ZT14 CHICK
 ID Q7ZT14_CHICK PRELIMINARY; PRT; 347 AA.
 AC Q7ZT14;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
 DE Growth hormone secretagogue receptor type 1a.
 GN Name=Ghr; Synonym=Ghsr1a;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=white leghorn; TISSUE=Kidney, and Pituitary;
 RX MEDLINE=22874039; PubMed=14511992; DOI=10.1016/S0016-6480(03)00247-8;
 RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsushima N.,
 RA Wakita M., Shimada K.;

RT "Molecular characterization of chicken growth hormone secretagogue
 receptor gene,";
 RT Gen. Comp. Endocrinol. 134:198-202(2003).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AB095995; BAC76444.1; -; mRNA.
 DR EMBL; AB095994; BAC76443.1; -; Genomic DNA.
 DR Ensembl; ENSGALG0000009187; Gallus gallus.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003905; GHS1_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01417; GHSRECEPTOR.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 347 AA; 39439 MW; 7A7543A9A4222F4 CRC64;

Query Match 74.1%; Score 1411; DB 2; Length 347;
 Best Local Similarity 76.5%; Pred. No. 5.4e-91;
 Matches 264; Conservative 37; Mismatches 44; Indels 0; Gaps 0;

QY 22 DASPGNDLGLDELQLPAPLAGVATCTVALFVVGIAAGNLLTMLVVSRRFELRTTNLY 81
 DB 3 EGSENRGTGSGPLRLPAPVLTGTVACVLLFVVGVLGNLMTLWVSFRFDMRTTTFY 62

QY 82 LSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSECTVATVLTALSVER 141
 DB 63 LSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSECTVLTILNITALSVER 122

QY 142 YFAICFPLRAKVVTGKRVKLVIVIVAVAFCSAGPIFVLVGVHENGCTDPDWTNECRPT 201
 DB 123 YVACFPLRAKVITTKRVKLVILWAVSFISAGPIFVLVGVHENGNTPLSTNECRAT 182

QY 202 EFAVRSGLLTVMWVSSIFFPVFCITVLYSLIGRKLWRRRRGDVAVVGASLRDQNHQK 261
 DB 183 EYAIRSGLLTVMWISSIFFPVFCITVLYSLIGRKLWRRKKNIGSTIIRDKNNQOT 242

QY 262 VKMLAVVVFAPILCWLPHFVGRYLFKSFPGSLEIAQISOYCNLVSEVLYFYLGAANPIL 321
 DB 243 VKMLVWVVFAPILCWLPHFVGRYLFKSFPAGSLEIAVISOYCNLVSEVLYFYLGAANPIL 302

QY 322 LYNIIMSKKYRVAVFRLGFPFSPQRKSLTKDESSRAWTESSINT 366
 DB 303 LYNIIMSKKYRVAAACRLFGKLPKRSLSTKQDSRWVTEPTVAT 347

RESULT 8
 Q6ISR8 HUMAN
 ID Q6ISR8_HUMAN PRELIMINARY; PRT; 289 AA.
 AC Q6ISR8;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE Growth hormone secretagogue receptor, isoform 1b.
 GN Name=GHSR;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones, and Synthetic constructs;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synthetic constructs;
RG NIH MGC Project;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; BC069374; AAH69374.1; -; mRNA.
DR EMBL; BC069068; AAH69068.1; -; mRNA.
DR Ensembl; ENSG00000121853; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:g-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007186; P:g-protein coupled receptor activity; IEA.
DR GO; GO:0007186; P:g-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 289 AA; 32153 MW; 8032FDB4C6BDD42B CRC64;

Query Match 72.9%; Score 1388; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWATPSEEPGNLTADLDWDASPGNDSLGDELQLFPAPLLAGVTATCVLPVVGVIAG 60
DB 1 MNWATPSEEPGNLTADLDWDASPGNDSLGDELQLFPAPLLAGVTATCVLPVVGVIAG 60

QY 61 NLLTMLVVSREPRETTNLYLSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
DB 61 NLLTMLVVSREPRETTNLYLSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120

QY 121 FVSESCYATVLTITALSVERFYFAICFPLRAKVVTGRVKLVFIWAVAFCSAGPIFV 180
DB 121 FVSESCYATVLTITALSVERFYFAICFPLRAKVVTGRVKLVFIWAVAFCSAGPIFV 180

QY 181 LVGVEHNGTDPWDTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLW 240
DB 181 LVGVEHNGTDPWDTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLW 240

QY 241 RRRRGDAVVGASLRDQNHKQTVKML 265
DB 241 RRRRGDAVVGASLRDQNHKQTVKML 265

RESULT 9
Q7ZZJ9 CHICK
ID Q7ZZJ9 CHICK PRELIMINARY; PRT; 331 AA.
AC Q7ZZJ9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type Ia variant.
GN Name=Ghst1av;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RX MEDLINE=22874039; PubMed=14511992; DOI=10.1016/S0016-6480(03)00247-8;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsushima N.,
RA Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
RT receptor gene";
RL Gen. Comp. Endocrinol. 134:198-202 (2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AB095996; BAC76445.1; -; mRNA.
DR Ensembl; ENSGALG0000009187; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:g-protein coupled receptor activity; IEA.
DR GO; GO:0007186; P:g-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007186; P:g-protein coupled receptor activity; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 331 AA; 37568 MW; 1BE477BF2D7A3BEB CRC64;

Query Match 68.7%; Score 1308; DB 2; Length 331;
Best Local Similarity 72.2%; Pred. No. 8.6e-84;
Matches 249; Conservative 37; Mismatches 43; Indels 16; Gaps 1;

QY 22 DASPGNDSLGDELQLFPAPLLAGVTATCVLPVVGVIAGVTATCVLPVVGVIAG 81
DB 3 EGSSENRTGSEPLRLFPAPLVATGTVACVLLFVVGVLGNLMTMLVVSFRDMRTTNFY 62

QY 82 LSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSECTATVLTITALSVER 141
DB 63 LSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSECTATVLTITALSVER 122

QY 142 YFAICFPLRAKVVTGRVKLVFIWAVAFCSAGPIFVLVGVGHEHNGTDPWDTNECRPT 201
DB 123 YVAICFPLRAKVVTGRVKLVFIWAVAFCSAGPIFVLVGVGHEHNGTDPWDTNECRPT 182

QY 202 EFVAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLWRRRGDAVVGASLRDQNHKQT 261
DB 183 EYAIRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLWRRRGDAVVGASLRDQNHKQT 242

QY 262 VKMLAVVVFVAFILCWLPFFHGVRLFSKSPGSLIAIQISQYCNLVSVFLYLSAAINPI 321
DB 243 VKML-----GRYLFKSPGSLIAIQISQYCNLVSVFLYLSAAINPI 296

QY 322 LYNNIMSKYRVAVRLLGPFPFGRKLTSLTKDESSRAWTESSINT 366
DB 287 LYNNIMSKYRVAVRLLGPFPFGRKLTSLTKDESSRAWTESSINT 331

RESULT 10
Q6YG23 ACASC
ID Q6YG23 ACASC PRELIMINARY; PRT; 385 AA.
AC Q6YG23;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Growth hormone secretagogue receptor 1a.
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;
RA Chan C.B., Cheng C.H.K.;
RT "Identification and functional characterization of two alternatively
spliced growth hormone secretagogue receptor transcripts from the
pituitary of black seabream Acanthopagrus schlegelii.";
RL Mol. Cell. Endocrinol. 214:81-95(2004).
CC -/- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -/- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; AV151040; AN77875.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; P:signal transduction; IEA.
DR InterPro; IPR0001765; P:signal transduction; IEA.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 385 AA; 43697 MW; 655CBDA9702887A9 CRC64;

Query Match 58.0%; Score 1105; DB 2; Length 385;
Best Local Similarity 56.2%; Pred. No. 1.7e-69;
Matches 216; Conservative 59; Mismatches 73; Indels 36; Gaps 5;

QY 2 WNAIPSEEGFNLTADLDWDASPGNDSLGDELQLFPAPLAGVATATCVAFVVGIAGN 61
DB 17 WEETRNATKFDGLPLNY-----YSIPLTGITIACTLLFLVGAGN 60
QY 62 LITMLVVSFRRLRTTNLYLSMAFSDLLIFLCPLDLVRLVQYRPNWFGDLCKLQF 121
DB 61 VMTILVSKYRDRTTNLYLSMAVSDLLIFLCPLDLVRLVQYRPNWFGDLCKLQF 120
QY 122 VSESCYATVLTALSVERVFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFVL 181
DB 121 VSESCYATVLTALSVERVFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFVL 180
QY 182 VGVHEH-----NGT-----DPWTNCRPTFEFAVRSGLLTVMWVSSIFFFLPV 225
DB 181 VGVVERDSMPGNLSWGMNGTGFFPEEGDTRECKMTHAVESGLMGAMVWLSVFFMPV 240
QY 226 FCILTLYSLIGRLRRRRGDAVG-ASLRDQNHQTVKMLAVVFAFLICWLPHVGRY 284
DB 241 FCILTLYSLIGRLRRRRGDAVG-ASLRDQNHQTVKMLAVVFAFLICWLPHVGRY 300
QY 285 LFSKSPFSGLEIAQISOYCNLSVFLFYLISAAINPILYNIMSKYKRVAVFRLGFG--- 341
DB 301 LQFRSLDAPSLLSLEYCSLVSVVFLYLSAAINPILYNIMSKYKRVAVFRLGFG--- 340
QY 342 PFSQRLSTLKDESSRAWTESSIN 365
DB 361 PPRGRSTASTKVGDSNGWTESTIS 384

Db 361 TVRMD---GWTESTVS 373

RESULT 12

Q4STY3 TETNG

ID Q4STY3 TETNG PRELIMINARY; PRT; 394 AA.

AC Q4STY3;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Chromosome 10 SCAF14066, whole genome shotgun sequence.

DE (Fragment).

GN ORFNames=GSTENG00012720001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=99883;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Aihouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

RT the early vertebrate proto-karyotype.";

RL Nature 431:946-957(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC ENBL: CAAE01014066; CAP95899.1; -; Genomic_DNA.

DR InterPro: IPR003905; GHS1_receptor.

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR01417; GHSRECEPTOR.

DR PRINTS: PR00237; GPCR_RHODOPSIN.

DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.

DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL 2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

FT NON TER 394

SQ SEQUENCE 394 AA; 44317 MW; EBC6972602B8861D CRC64;

Query Match 56.5%; Score 1075.5; DB 2; Length 394;

Best Local Similarity 57.9%; Pred. No. 26-67;

Matches 220; Conservative 53; Mismatches 82; Indels 25; Gaps 8;

QY 4 ATPSEEPGNLTADLDW--DASPGNDSLGDE--LLQLFPAPLAGVATATCVALLFVVGAG 60

DB 21 ATCSAPVCPATAA--WRRATTPRGALSSKCHLLITQIPLLAVITACTVLTFTGVVG 77

QY 61 NLITMLVVSFRLETTNNLYLSMAFSDLLIFLCMPDLVRLWQYRPWPNFGDLLCKLFQ 120

DB 78 NVMTILVVSRYRDMRTTNNLYLSMAVSDLFIFVCMPLDLRYMRWRPWRFGDALKCFQ 137

QY 121 FVSECTYATVLTALTSVRYFAICPLRAKVVTGKRVKLVIFVWAVAFCSAGPIFV 180

DB 138 FVSECTYSTILCTALTSVRYLAICPLRAKALVTKRRVRALLTLTLLVTSLSAGVFFV 197

QY 181 LVGVHEB-----NCTDPMDTNECRTEPAFVRSGLLTVMVWVSSIFFFLPVPFCLT 229

DB 198 MVGVSRDSIPTNTFTSEKNGSAE-DTRECMTQFAVESGLMEAMVWVLSVFFFPVFCLT 256

QY 230 VLYSLIGRKLWRRRRGDVAVG-ASLRDNHKOITVKMLAVVVFVAFILCWLPHVCRYLFSK 288

DB 257 VLYSLIGRRLWLRRHRETSINSRVAYRDKSNROTICKMLVVVLAFLCWLPHVGRYLFQR 316

QY 289 SFEPGSLIEIAISOYCNLVSVFLFYLSAALNPILYNTMSKRYVAVFRLILGF---EPFSQ 345

DB 317 SLDAPSPILLSLEYCSLVSVFLFYLSAALNPILYNTMSKRYGAVARLFGVSDGHQFQR 376

QY 346 RKLSTLKDESSRAWTESSIN 365

DB 377 RTASTVKGD---GWTESTVS 393

RESULT 13

Q7ZZJ8 CHICK

ID Q7ZZJ8 CHICK PRELIMINARY; PRT; 267 AA.

AC Q7ZZJ8;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Growth hormone secretagogue receptor type 1b.

GN Name=Ghsrlb;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=white leghorn; TISSUE=Pituitary;

RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.,

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC ENBL: AB095997; BAC76446.1; -; mRNA.

DR Ensembl: ENSGALG0000009187; Gallus gallus.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0016220; F:growth hormone-releasing hormone receptor a. . . ; IEA.

DR GO: GO:0004872; F:receptor activity; IEA.

DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO: GO:0007165; P:signal transduction; IEA.

DR InterPro: IPR003905; GHS1_receptor.

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR01417; GHSRECEPTOR.

DR PRINTS: PR00237; GPCR_RHODOPSIN.

DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.

DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL 2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

FT NON TER 267

SQ SEQUENCE 267 AA; 30209 MW; 00563690B35AD107 CRC64;

Query Match 53.0%; Score 1010; DB 2; Length 267;

Best Local Similarity 74.3%; Pred. No. 5.4e-63;

Matches 188; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

QY 22 DASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGAGVATATCVALLFVVGAG 81

DB 3 EGSSSENRTGSGSLRLLFPAPLVGTITVACVLLFVVGVLGNLMTMLVVSFRDMRTTNNFY 62

QY 82 LSSMAFSDLLIFLCMPDLVRLWQYRPWPNFGDLLCKLFQFVSECTYATVLTALTSVER 141

DB 63 LSSMAFSDLLIFLCMPDLVRLWQYRPWPNFGDLLCKLFQFVSECTYATVLTALTSVER 122

QY 142 YFAICPLRAKVVTGKRVKLVIFVWAVAFCSAGPIFVWAVAFCSAGPIFVWAVAFCSAGPIFV 201

DB 123 YVAICPLRAKVVTGKRVKLVILWVAFISAGPIFVWVGVHEHNGTNPLSTNECRAT 182

QY 202 EFVRSGLLTVMVWVSSIFFFLPVPFCLTLYLSLIGRKLWRRRRGDVAVGASLRDNHKOIT 261

```
Db 183 EYAIRSGLLTINWVLISSIFFFLPVCLTVLSLGRKLRKRNKNGIFSTIIRDKNKQT 242
QY 262 VKMLAVVVFAPFL 274
Db 243 VKMLGMAPRALCL 255

RESULT 14
Q711Q7 CHICK
ID Q711Q7 CHICK PRELIMINARY; PRT; 215 AA.
AC Q711Q7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Putative growth hormone secretagogue receptor 1a (Fragment).
GN Name=GHS1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypothalamus;
RX MEDLINE=22874034; PubMed=14511987; DOI=10.1016/S0016-6480(03)00250-8;
RA Geelissen S.M.E., Beck I.M.E., Darras V.M., Kuhn E.R.,
RA Van der Gayten S.;
RT "Distribution and regulation of chicken growth hormone secretagogue
RT receptor isoforms.";
RL Gen. Comp. Endocrinol. 134:167-174(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AJ309543; CAC29062.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCRKHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 24487 MW; 68BCE14DFE81DEF5 CRC64;

Query Match 45.7%; Score 871; DB 2; Length 215;
Best Local Similarity 75.3%; Pred. No. 2.5e-53;
Matches 165; Conservative 19; Mismatches 19; Indels 16; Gaps 1;

QY 102 RLWQYRPNFQDLCKLQFQVSESTYATVLTITALSVERFYAICFPLRAKVVTYKRVK 161
Db 1 RLWQYRPNFQDLCKLQFQVSESTYATVLTITALSVERFYAICFPLRAKVVTYKRVK 60

QY 162 LVIFVIAVAFCSAGPIFVLGVHENGTDPDNTNECRPTFAVRSGLLTVMVWVSSIFF 221
Db 61 LVILILMAVSTFISAGPIFVLGVHENGTNPJLSTNECRATEYAIRSGLLTITMVISSIFF 120

QY 222 FLPVFCLTVLSLGRKLRRRRRGDVAVGASLRDQNHQTVKMLAVVVFATFCLWLPFHV 281
Db 121 FLPVFCLTVLSLGRKLRKRNKNGIFSTIIRDKNKQTVMU----- 164

QY 282 GRYLFSKFEFGSLBIAIQSVCNLVSVFLVFLSAINP 320
Db 165 GRYLFSKFEAGSLBIAIVISQCNLVSVFLVFLSAATP 203
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RESULT 15
MTLR_HUMAN
ID MTLR_HUMAN STANDARD; PRT; 412 AA.
AC O43193;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Motilin receptor (G-protein coupled receptor 38).
GN Name=MLNR; Synonyms=GPR38, MTLR, MTLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM A).
RX MEDLINE=98110578; PubMed=9441746; DOI=10.1006/geno.1997.5069;
RA McKee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,
RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;
RT "Cloning and characterization of two human G protein-coupled receptor
RT genes (GPR38 and GPR39) related to the growth hormone secretagogue and
RT neurotensin receptors.";
RL Genomics 46:426-434(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS A AND B).
RX MEDLINE=99316084; PubMed=10381885; DOI=10.1126/science.284.5423.2184;
RA Feighner S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk D.L.,
RA Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.,
RA Nargund R., Bakhshi R., Abramovitz M., Stocco R., Kargman S.,
RA O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,
RA Howard A.D.;
RT "Receptor for motilin identified in the human gastrointestinal
RT system.";
RL Science 284:2184-2188(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM A).
RC TISSUE=Stomach;
RA King M.W., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15057823; DOI=10.1038/nature02379;
RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,
RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
RA Ashwell R.I.S., Babbage A.K., Bagguley C.L., Bailey J., Bannerjee R.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Deloukas P., Dhami P., Dunham I., Dunn M., Earthworn M.E.,
RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,
RA Hunt P.J., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
RA Hunt A.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,
RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,
RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Sehra H.K., Showkneen R., Skuce C.D., Smith M., Steward C.A.,
RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA Hubbard T., Stulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.;
RT "The DNA sequence and analysis of human chromosome 13.";
RL Nature 428:522-528(2004).
RN [5]
RP FUNCTION.
```


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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:23:48 ; Search time 205.354 Seconds
(without alignments)
783.099 Million cell updates/sec

Title: US-09-718-803A-5
Perfect score: 1905
Sequence: 1 MWNA TPSEPGFNLTLADLD.....KSLTKDESGRAWTESSINT 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1905	100.0	366	3 AAY70345	Aay70345 Human G p
2	1905	100.0	366	3 AAY90632	Aay90632 Human G p
3	1905	100.0	366	4 AAB97376	Aab97376 Rat growt
4	1905	100.0	366	4 AAB62650	Aab62650 Human G-p
5	1905	100.0	366	5 ABB09534	Abb09534 Human ghr
6	1905	100.0	366	7 ADC22607	Adc22607 Human G p
7	1905	100.0	366	7 ADH14080	Adh14080 Human GHS
8	1905	100.0	366	8 ADD35398	Add35398 Human gro
9	1905	100.0	366	8 ADN12078	Adn12078 Protein #
10	1905	100.0	366	8 ADN11756	Adn11756 Human gro
11	1905	100.0	366	8 ADO29025	Ado29025 Human nov
12	1905	100.0	366	8 ADQ28857	Adq28857 Human ghr
13	1899	99.7	366	3 AAY90666	Aay90666 Human mut
14	1899	99.7	366	7 ADC22729	Adc22729 Human G p
15	1899	99.7	366	7 ADH14202	Adh14202 Murated h
16	1874	98.4	361	2 AAW19217	Aaw19217 Human gro
17	1874	98.4	362	2 AAW19610	Aaw19610 Human gro
18	1789	93.9	364	4 AAB97377	Aab97377 Rat growt
19	1788	93.9	364	3 AAY54565	Aay54565 A mouse g
20	1788	93.9	364	8 ADO29026	Ado29026 Mouse nov
21	1782	93.5	364	2 AAW19613	Aaw19613 Rat growt
22	1770	92.9	364	2 AAW19220	Aaw19220 Rat growt
23	1713.5	89.9	705	8 ADU82862	Adu82862 Ligand up
24	1704	89.4	353	2 AAW19215	Aaw19215 Swine gro

25	1704	89.4	353	2 AAW19608	Aaw19608 Pig growt
26	1596.5	83.8	349	3 AAY69293	Aay69293 A canine
27	1418	74.4	271	2 AAW19219	Aaw19219 Human gro
28	1418	74.4	271	2 AAW19612	Aaw19612 Human gro
29	1388	72.9	289	2 AAW19611	Aaw19611 Human gro
30	1388	72.9	289	6 ABP81828	Abp81828 Human gro
31	1383	72.6	289	2 AAW19218	Aaw19218 Human gro
32	1266	66.5	289	2 AAW19216	Aaw19216 Swine gro
33	1266	66.5	289	2 AAW19609	Aaw19609 Pig growt
34	874.5	45.9	400	4 AAB68477	Aab68477 Amino aci
35	863.5	45.3	412	3 AAY54145	Aay54145 Amino aci
36	863.5	45.3	412	4 AAB68478	Aab68478 Amino aci
37	863.5	45.3	412	4 AAB62652	Aab62652 Long form
38	863.5	45.3	412	5 ABG30936	Abg30936 Human G p
39	863.5	45.3	412	6 ABP81993	Abp81993 Human mot
40	863.5	45.3	412	8 ADN11761	Adn11761 Human mot
41	863.5	45.3	412	8 ADO29697	Ado29697 Human GPC
42	863.5	45.3	412	8 ADQ37921	Adq37921 Human G-p
43	863.5	45.3	501	4 AAG65822	Aag65822 Human GPR
44	862	45.2	363	3 AAY54147	Aay54147 The pufte
45	862	45.2	363	4 AAB68479	Aab68479 Amino aci

ALIGNMENTS

RESULT 1
AAY70345
ID AAY70345 standard; protein; 366 AA.
XX
AC AAY70345;
XX
DT 20-JUN-2000 (first entry)
XX
DE Human G protein-coupled orphan receptor, GHSR.
XX
KW G protein-coupled orphan receptor; GPCR; agonist; G protein; treatment;
KW GPCR fusion protein; inverse agonist; drug; GHSR; human.
XX
OS Homo sapiens.
XX
PN W0200006597-A2.
XX
PD 10-FEB-2000.
XX
PF 30-JUL-1999; 99WO-US017425.
XX
PR 31-JUL-1998; 98US-0094879P.
PR 30-OCT-1998; 98US-0106300P.
PR 04-DEC-1998; 98US-0110906P.
PR 26-FEB-1999; 99US-0121851P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Chalmers DT, Liaw C, Lin I, Lowitz K, Chen R;
XX
DR WPI; 2000-195260/17.
XX
N-PSDB; AAZ51463.
XX
PT Identification of a compound useful as a therapeutic agent, comprises
PT identifying a compound against constitutively activated G protein-coupled
PT orphan receptors.
XX
PS Example 2; Page 123; 123pp; English.
XX
CC The patent discloses a method of identifying agonists and inverse or
CC partial agonists to the endogenous, constitutively activated G protein-
CC coupled orphan receptors (GPCRs), by contacting them with a GPCR fusion
CC protein comprising a GPCR and a G protein. Determining expression of
CC GPCRs in tissue samples can be used to identify related diseases. Inverse
CC agonists to these receptors can be used as drugs for treating GPCR-
CC related diseases. The present protein sequence is that of human G protein
CC -coupled orphan receptor, GHSR

```

XX Sequence 366 AA;
SQ
Query Match 100.0%; Score 1905; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
DB 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
QY 61 NLLTMLVVSFRRELTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILCKLFQ 120
DB 61 NLLTMLVVSFRRELTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILCKLFQ 120
QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
QY 181 LVGVEHNGTDPWDNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCITVLYSLGRKLM 240
DB 181 LVGVEHNGTDPWDNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCITVLYSLGRKLM 240
QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPFSGSLEIAQI 300
DB 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPFSGSLEIAQI 300
QY 301 SQYCNLVSFVLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360
DB 301 SQYCNLVSFVLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366
RESULT 2
AA90632
ID AA90632 standard; protein; 366 AA.
AC AA90632;
XX 21-AUG-2000 (first entry)
DT Human G protein-coupled receptor GHSR.
DE G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
KW antagonist.
XX Homo sapiens.
OS
XX WO200022129-A1.
XX 20-APR-2000.
XX 12-OCT-1999; 99WO-US023938.
XX 13-OCT-1999; 98US-00170496.
XX (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw CW;
XX WPI; 2000-329165/28.
XX N-PSDB; AAA30643.
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents.
XX Example 1; Page 167-169; 341pp; English.
XX

```

```

CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AA90643-
CC AA90677 and AA90683-190687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
CC Ala, and is preferably Lys. When the endogenous residue at this position
CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
CC amino acid stretch between the substituted amino acid and the Pro may be
CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. The present sequence
CC represents a human wild-type GPCR referred to in an exemplification of
CC the invention
XX
SQ Sequence 366 AA;
Query Match 100.0%; Score 1905; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
DB 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
QY 61 NLLTMLVVSFRRELTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILCKLFQ 120
DB 61 NLLTMLVVSFRRELTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILCKLFQ 120
QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
QY 181 LVGVEHNGTDPWDNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCITVLYSLGRKLM 240
DB 181 LVGVEHNGTDPWDNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCITVLYSLGRKLM 240
QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPFSGSLEIAQI 300
DB 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPFSGSLEIAQI 300
QY 301 SQYCNLVSFVLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360
DB 301 SQYCNLVSFVLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366
RESULT 3
AA907376
ID AA907376 standard; protein; 366 AA.
XX AA907376;
XX 16-AUG-2001 (first entry)
DT Rat growth hormone secretagogue receptor (GHSR) related protein.
DE Growth hormone secretagogue receptor; GHSR; GHSR ligand; nootropic;
XX antiarthritic; cytostatic; antidiabetic; pituitary dwarfism;
KW Turner's syndrome; chronic nephritis; chondrodystrophy; Down's syndrome;
KW Silver syndrome; bone formation disorder; juvenile chronic arthritis;
KW

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KW megacephalia; tumour; insulinoma; calcinoid; diabetes; rat.
 OS Rattus sp.
 XX WO200132705-A1.
 XX PD 10-MAY-2001.
 XX PF 31-OCT-2000; 2000WO-JP007635.
 XX PR 01-NOV-1999; 99JP-00311632.
 XX PR 17-DEC-1999; 99JP-00358723.
 XX XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX XX
 XX PI Hinuma S, Kawamata Y, Fukusumi S, Fujii R;
 XX WPI; 2001-308741/32.
 XX XX
 XX Growth-hormone secretagogue receptor ligand polypeptides and encoded
 XX DNAs, useful in diagnosis and screening drug candidates for treating e.g.
 XX PT pituitary dwarfism, Turner syndrome, chronic nephritis.
 XX PS
 XX Claim 14; Page 90-92; 106pp; Japanese.
 XX XX
 CC This invention relates to a growth hormone secretagogue receptor (GHSR)
 CC ligand peptide. The invention contains bovine, human, rat and porcine
 CC GHSR gene and protein sequences, and also GHSR ligand sequences. The use
 CC of an antibody directed against GHSR ligand, GHSR promoters and
 CC inhibitors may lead to nootropic, antiarthritic, cytostatic, and
 CC antidiabetic activity. GHSR DNA, protein, promoters and inhibitors are
 CC useful for preventing or treating diseases caused by insufficient growth
 CC hormone, e.g. pituitary dwarfism, Turner syndrome, chronic nephritis,
 CC chondrodystrophy, adult pituitary failure, Down's syndrome, Silver
 CC syndrome, bone formation disorder, juvenile chronic arthritis syndrome or
 CC for diseases of megacephalia, thyroid stimulating hormone (TSH)-promoting
 CC tumours, non-secretory (non-functional) pituitary tumours, ectopic
 CC adrenocorticotrophic hormone (ACTH)-producing tumours, myeloid thryoma,
 CC vasotrophic inhibitory peptide (VIP)-producing tumours, glucagon-producing
 CC tumour, gastrin-producing tumour, insulinoma, calcinoid, insulin-
 CC dependent or non-dependent diabetes. The present sequence represents rat
 CC GHSR-related protein
 XX
 SQ Sequence 366 AA;

Query Match 100.0%; Score 1905; DB 4; Length 366;
 Best Local Similarity 100.0%; Pred. No. 1.3e-200; Indels 0; Gaps 0;
 Matches 366; Conservative 0; Mismatches 0;

Qy 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
 Db 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60

Qy 61 NLLTMLVVSRRPRELRTTNLYLSSNAFSDLLIFLCMLDLVRLWQYRPNFPGDLLCKLFQ 120
 Db 61 NLLTMLVVSRRPRELRTTNLYLSSNAFSDLLIFLCMLDLVRLWQYRPNFPGDLLCKLFQ 120

Qy 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVTGRVKLVIFVWAVAFCSAGPIFV 180
 Db 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVTGRVKLVIFVWAVAFCSAGPIFV 180

Qy 181 LVGVEHNGTDPDWTNECRPTEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 240
 Db 181 LVGVEHNGTDPDWTNECRPTEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 240

Qy 241 RRRRGDAVVGASLRQNHQKQVWMLAVVVFALICWLPFHVGRYLFKSPFGSLEIAQI 300
 Db 241 RRRRGDAVVGASLRQNHQKQVWMLAVVVFALICWLPFHVGRYLFKSPFGSLEIAQI 300

Qy 301 SOYCNLVSVFLFYLSAANPILYNIMSKYRVAVFRLLGPEPFSQKSLTKDESSRAWT 360
 Db 301 SOYCNLVSVFLFYLSAANPILYNIMSKYRVAVFRLLGPEPFSQKSLTKDESSRAWT 360

Qy 361 ESSINT 366
 Db 361 ESSINT 366

RESULT 4
 AAB62650
 ID AAB62650 standard; protein; 366 AA.
 XX AC AAB62650;
 XX DT 23-JUL-2001 (first entry)
 XX XX
 XX Human G-protein coupled receptor, GHS-R.
 XX DE
 XX KW zsig33; signal transduction; hormone; enzyme; neural development;
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
 KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 KW G-protein coupled receptor.
 XX OS Homo sapiens.
 XX PH
 XX Key Location/Qualifiers
 FT Domain 1..40
 FT /note= "extracellular domain"
 FT Domain 41..66
 FT /note= "transmembrane alpha-helix 1"
 FT Domain 67..72
 FT /note= "cytoplasmic fragment"
 FT Domain 73..96
 FT /note= "transmembrane alpha-helix 2"
 FT Domain 97..117
 FT /note= "extracellular domain"
 FT Domain 118..139
 FT /note= "transmembrane alpha-helix 3"
 FT Domain 140..162
 FT /note= "cytoplasmic fragment"
 FT Domain 163..183
 FT /note= "transmembrane alpha-helix 4"
 FT Domain 184..211
 FT /note= "extracellular domain"
 FT Domain 212..235
 FT /note= "transmembrane alpha-helix 5"
 FT Domain 236..263
 FT /note= "cytoplasmic fragment"
 FT Domain 264..285
 FT /note= "transmembrane alpha-helix 6"
 FT Domain 286..302
 FT /note= "extracellular domain"
 FT Domain 303..326
 FT /note= "transmembrane alpha-helix 7"
 FT Domain 327..326
 FT /note= "cytoplasmic fragment"
 XX PN WO200138355-A2.
 XX PD 31-MAY-2001.
 XX PF 22-NOV-2000; 2000WO-US032074.
 XX PR 22-NOV-1999; 99US-0166765P.
 XX XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX XX
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 XX WPI; 2001-355879/37.
 XX DR N-PSDB; AAF83680.
 XX XX
 XX Forming reversible peptide receptor complex for purifying cell and
 XX peptides, stimulating signal transduction and modulating hormone
 XX secretion, involves contacting a receptor with zsig33 polypeptide.

XX Claim 2; Page 95-98; 11pp; English.

PS The invention relates to a method of forming a reversible peptide-

XX receptor complex that involves providing an immobilized receptor, and

CC contacting the receptor with a zsig33 peptide (comprising residues 24-37

CC of AAB62649), where the receptor binds to the zsig33 peptide. The method

CC is useful for purifying cells, purifying a peptide, stimulating signal

CC transduction in a cell expressing a receptor. It is also useful for

CC modulating secretion of hormones, neural development and/or utilization,

CC gastric contractility, nutrient uptake, secretion of digestive and

CC pancreatic enzymes and hormones, secretion of insulin-like growth factor

CC -1, secretion of non-zsig33 proteins. It is useful for modulating growth

CC hormone secretion in a mammal having a disease associated with abnormal

CC levels of growth hormone, such as osteoporosis, bone repair, bone

CC remodeling, low osteoblast levels, cartilage repair and remodeling,

CC skeletal dysplasia, immune suppression, obesity, growth retardation,

CC protein catabolic responses after surgery, cachexia, protein loss,

CC dwarfism, wound healing and ovulation induction, treating a mammal having

CC a metabolic disorder requiring neurological feedback, such as satiety

CC regulation, glucose absorption and metabolism and neuropathy-associated

CC gastrointestinal disorders, and stimulating glucose-induced insulin

CC release in a mammal. The present sequence represents the human G-protein

CC coupled receptor, GHS-R, to which the zsig33 peptide binds to

XX

SQ Sequence 366 AA;

Query Match 100.0%; Score 1905; DB 4; Length 366;

Best Local Similarity 100.0%; Pred. No. 1.3e-200;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNATPSEPGFNLTADLDWDASFGNDSLGDELLQLPAPLAGVTATCVAFVVGAG 60

DB 1 MNNATPSEPGFNLTADLDWDASFGNDSLGDELLQLPAPLAGVTATCVAFVVGAG 60

QY 61 NLLTMLVSVRFRELTNTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLPQ 120

DB 61 NLLTMLVSVRFRELTNTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLPQ 120

QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVCLVFIWAVAFCSAGPIFV 180

DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVCLVFIWAVAFCSAGPIFV 180

QY 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCLTVLSLGRKLW 240

DB 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCLTVLSLGRKLW 240

QY 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFSSKFEFGSLEIAQI 300

DB 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFSSKFEFGSLEIAQI 300

QY 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360

DB 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360

QY 361 ESSINT 366

DB 361 ESSINT 366

RESULT 5

ABB09534

ID ABB09534 standard; protein; 366 AA.

XX

XX ABB09534;

XX

XX 22-OCT-2002 (first entry)

DT Human ghrelin receptor (GHSR, growth hormone secretagogue receptor).

DE Human; ghrelin receptor; appetite; food intake; agonist; analogue;

XX Human; ghrelin receptor; appetite; food intake; agonist; analogue;

XX undernutrition; anorexia; cachexia; malignant disease; infection;

XX inflammatory disease; weight loss; antagonist; obesity; anorectic;

KW anabolic; GHSR; growth hormone receptor; GHSR; receptor.

XX Homo sapiens.

XX WO200260472-A1.

PD 08-AUG-2002.

PF 31-JAN-2002; 2002MO-JP0000765.

PR 31-JAN-2001; 2001JP-00024423.

PA (CHUS) CHUGAI SEIYAKU KK.

XX Inui A, Asakawa A, Kaga T;

XX WPI; 2002-619206/66.

DR Remedies for diseases with hypo-nutrition status e.g. inappetence and

PT cachexia, containing ghrelin or its analogs including agonists and

PT antagonists.

XX Disclosure; Fig 1B; 50pp; Japanese.

XX The invention relates to the use of ghrelin or its analogues for the

CC treatment of diseases associated with undernutrition such as anorexia,

CC and also relates to the use of ghrelin antagonists for the prevention or

CC treatment of obesity. The invention additionally discloses a method for

CC screening ghrelin agonists or antagonists by measuring the amount of food

CC intake, neuropeptide Y (NPY) expression, binding of NPY to NPY receptor

CC Y1, oxygen consumption, gastric emptying, or activity of the vagus nerve.

CC Intracerebroventricular (ICV) administration of ghrelin in animals was

CC found to increase food intake over a period of 24 hours. Ghrelin and its

CC analogues may therefore be used to treat conditions such as loss of

CC appetite, anorexia, cachexia, malignant diseases, and weight loss

CC associated with infection or inflammatory diseases. Conversely, ghrelin

CC antagonists may be used in the treatment of obesity. The present sequence

CC represents the human ghrelin receptor (also known as growth hormone

CC secretagogue receptor, or GHSR) which is referred to in the disclosure of

XX the invention

SQ Sequence 366 AA;

Query Match 100.0%; Score 1905; DB 5; Length 366;

Best Local Similarity 100.0%; Pred. No. 1.3e-200;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNATPSEPGFNLTADLDWDASFGNDSLGDELLQLPAPLAGVTATCVAFVVGAG 60

DB 1 MNNATPSEPGFNLTADLDWDASFGNDSLGDELLQLPAPLAGVTATCVAFVVGAG 60

QY 61 NLLTMLVSVRFRELTNTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLPQ 120

DB 61 NLLTMLVSVRFRELTNTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLPQ 120

QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVCLVFIWAVAFCSAGPIFV 180

DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVCLVFIWAVAFCSAGPIFV 180

QY 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCLTVLSLGRKLW 240

DB 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCLTVLSLGRKLW 240

QY 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFSSKFEFGSLEIAQI 300

DB 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFSSKFEFGSLEIAQI 300

QY 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360

DB 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360

QY 361 ESSINT 366

DB 361 ESSINT 366

Db 361 ESSINT 366

RESULT 6

ADC22607

ID ADC22607 standard; protein; 366 AA.

AC ADC22607;

XX

XX 18-DEC-2003 (first entry)

XX

XX Human G protein-coupled receptor (GPCR) polypeptide #24.

XX

XX Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;

KW intracellular-3 region; IC3; receptor.

XX

XX Homo sapiens.

XX US655339-B1.

XX 29-APR-2003.

XX

XX 13-OCT-1998; 98US-00170496.

XX

PR 14-APR-1997; 97US-00839449.

PR 14-APR-1998; 98US-00060188.

PR 26-JUN-1998; 98US-0090783P.

PR 07-AUG-1998; 98US-0095677P.

XX

PA (AREN-) ARENA PHARM INC.

XX

XX Liaw CW, Behan DP, Chalmers DT;

PI

XX

DR WPI; 2003-742861/70.

DR N-PSDB; ADC22606.

XX

XX Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for constitutive activity.

XX

PS Example 1; SEQ ID NO 88; 221pp; English.

XX

CC The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the invention.

XX

SQ Sequence 366 AA;

Query Match 100.0%; Score 1905; DB 7; Length 366;

Best Local Similarity 100.0%; Pred. No. 1.3e-200;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWATPSEBGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGAG 60

DB 1 MNWATPSEBGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVALFVVGAG 60

QY 61 NLLTMLVVSFRPRELRTTTNLYLSSMAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 120

DB 61 NLLTMLVVSFRPRELRTTTNLYLSSMAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 120

QY 121 FVSESCYATVLTITALTALSVRYFAICFPLRAKVVVTKGRVKLVIFVIVAWAFCSAGPTFV 180

DB 121 FVSESCYATVLTITALTALSVRYFAICFPLRAKVVVTKGRVKLVIFVIVAWAFCSAGPTFV 180

QY 181 LVGVEHENGTDPMWDTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLVLSLIGRKLW 240

DB 181 LVGVEHENGTDPMWDTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLVLSLIGRKLW 240

QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFATILCWLPHFVGRYLFKSPFSGSLEIAQI 300

DB 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFATILCWLPHFVGRYLFKSPFSGSLEIAQI 300

QY 301 SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEPPSQKSLTKDESSRAWT 360

DB 301 SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEPPSQKSLTKDESSRAWT 360

QY 361 ESSINT 366

DB 361 ESSINT 366

RESULT 7

ADH14080

ID ADH14080 standard; protein; 366 AA.

XX

AC ADH14080;

XX

XX 11-MAR-2004 (first entry)

XX

XX Human GHSR.

XX

XX human; non-endogenous; G protein-coupled receptor; GPCR; receptor.

KW Homo sapiens.

XX

XX US2003105292-A1.

XX

XX 05-JUN-2003.

XX

XX 20-SEP-2002; 2002US-00251385.

XX

XX 26-JUN-1998; 98US-0090783P.

PR 07-AUG-1998; 98US-0095677P.

PR 13-OCT-1998; 98US-00170496.

XX

XX (LIAW/) LIAW C W.

PA (BEHA/) BEHAN D P.

PA (CHAL/) CHALMERS D T.

XX

XX Liaw CW, Behan DP, Chalmers DT;

PI

XX

XX WPI; 2003-801247/75.

DR N-PSDB; ADH14079.

XX

XX New constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor for the identification of therapeutic compounds, such as agonists.

XX

XX Example 1; SEQ ID NO 88; 227pp; English.

XX

CC The invention relates to a constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor (GPCR). The GPCR is used for screening therapeutic compounds as inverse agonists, agonists or partial agonists. The GPCR can be also used to elucidate and understand the roles of GPCRs in normal and diseased humans. The GPCR need not be purified and isolated to be used to screen for therapeutic compounds. The utility of the GPCR as a research tool is enhanced because the role of a particular receptor can be understood before the endogenous ligand is identified. The present sequence is used in the exemplification

CC	of the present invention.	PS	Disclosure; SEQ ID NO 2; 115pp; English.
XX		XX	
SQ	Sequence 366 AA;	CC	The invention relates to a novel method for screening for therapeutic agents useful in treating a disease consisting of cancer, respiratory diseases, genito-urinary diseases, haematological diseases, cardiovascular diseases or CNS diseases in a mammal. The method comprises contacting a test compound with a growth hormone secretagogue receptor (GHS) polypeptide, and detecting binding of the test compound to the GHS polypeptide. The method of the invention has cytostatic, cardiant, neuroprotective, respiratory, and gynaecological activity. The method is useful for screening for therapeutic agents for treating a disease consisting of cancer, respiratory diseases, genito-urinary diseases, haematological diseases, cardiovascular diseases or CNS diseases in a mammal. The present sequence represents the human GHS receptor of the invention.
QY	Query Match 100.0%; Score 1905; DB 7; Length 366; Best Local Similarity 100.0%; Pred. No. 1.3e-200; Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SQ	Sequence 366 AA;
QY	1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60	QY	1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
Db	1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60	Db	1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
QY	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQRPWNFGDLCKLFQ 120	QY	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQRPWNFGDLCKLFQ 120
Db	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQRPWNFGDLCKLFQ 120	Db	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQRPWNFGDLCKLFQ 120
QY	121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFV 180	QY	121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFV 180
Db	121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFV 180	Db	121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFV 180
QY	241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEPGSLKIAQI 300	QY	241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEPGSLKIAQI 300
Db	241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEPGSLKIAQI 300	Db	241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEPGSLKIAQI 300
QY	301 SOYCNLVSVFLPYLSAAINPILYNIMSKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360	QY	301 SOYCNLVSVFLPYLSAAINPILYNIMSKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360
Db	301 SOYCNLVSVFLPYLSAAINPILYNIMSKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360	Db	301 SOYCNLVSVFLPYLSAAINPILYNIMSKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360
QY	361 ESSINT 366	QY	361 ESSINT 366
Db	361 ESSINT 366	Db	361 ESSINT 366
RESULT 8		RESULT 9	
ADD35398		ADN12078	
ID	ADD35398 standard; protein; 366 AA.	ID	ADN12078 standard; protein; 366 AA.
AC	ADD35398;	XX	ADN12078;
XX		AC	ADN12078;
DT	15-JAN-2004 (first entry)	DT	17-JUN-2004 (first entry)
DE	Human growth hormone secretagogue receptor SEQ ID NO:2.	XX	
KW	human; growth hormone secretagogue receptor; GHS; cancer; respiratory; genito-urinary; haematological; cardiovascular; CNS; cytostatic; cardiant; neuroprotective; respiratory; gynaecological.	DE	Protein #3 associated with growth hormone secretagogue receptor.
XX		XX	diabetes; growth hormone secretagogue receptor; GHS-R; Antidiabetic; Anorectic; obesity; blood sugar level; appetite.
OS	Homo sapiens.	XX	Homo sapiens.
XX		OS	
PN	WO2003081258-A2.	XX	WO2004004772-A1.
XX		PN	
PD	02-OCT-2003.	XX	15-JAN-2004.
XX		PD	
PF	14-MAR-2003; 2003WO-BF002688.	XX	03-JUL-2003; 2003WO-JP008482.
XX		PF	
PR	26-MAR-2002; 2002EP-00006653.	XX	05-JUL-2002; 2002JP-00197582.
XX		PR	
PA	(FARB) BAYER AG.		
PI	Golz S, Brueggemeier U, Geerts A;		
XX			
DR	WPI: 2004-011536/01.		
DR	N-PSDB; ADD35397.		
XX			
PT	Screening for therapeutic agents for treating e.g., cancer in a mammal by contacting a test compound with a growth hormone secretagogue receptor (GHS) polypeptide and detecting binding of the test compound to the GHS polypeptide.		
XX			

```
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Inui A, Asakawa A;
XX XX
XX DR WPI; 2004-099347/10.
XX PT Growth hormone secretagogue receptor antagonist for treatment of
XX PT diabetes, obesity and appetite control.
XX PS Disclosure; SEQ ID NO 3; 44pp; Japanese.
XX XX
XX CC The present invention relates to a treatment and preventative agent for
XX CC diabetes comprises growth hormone secretagogue receptor (GHS-R)
XX CC antagonist. For treatment and prevention of diabetes, obesity, for
XX CC lowering blood sugar levels and for use in controlling appetite. The
XX CC present sequence represents a protein associated with growth hormone
XX CC secretagogue receptor.
XX SQ Sequence 366 AA;
Query Match 100.0%; Score 1905; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MWNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Db 1 MWNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Qy 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Db 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Qy 121 FVSESCYATVLTITALSVERVFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 180
Db 121 FVSESCYATVLTITALSVERVFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 180
Qy 181 LVGVEHENGTDPMWDTNECRPTFAVRSGLLTVMWVSSIFPFLPVFCLTVLYSLIGRKJL 240
Db 181 LVGVEHENGTDPMWDTNECRPTFAVRSGLLTVMWVSSIFPFLPVFCLTVLYSLIGRKJL 240
Qy 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Qy 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFEPPFSQKSLTLKDESSRAWT 360
Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFEPPFSQKSLTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366
RESULT 10
ADN11756
ID ADN11756 standard; protein; 366 AA.
XX XX
XX AC ADN11756;
XX XX
XX DT 15-JUL-2004 (first entry)
XX XX
XX DE Human growth hormone secretagogue GHS-R.
XX XX
XX KW human; zsig33; body weight; body mass; antibody; antagonist;
XX KW gastrointestinal; antiinflammatory; antidiabetic; antitumor;
XX KW growth hormone secretagogue; GHS-R; peptide-antibody complex.
XX OS Homo sapiens.
XX PN WO2004033645-A2.
XX PD 22-APR-2004.
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XX PF 06-OCT-2003; 2003WO-US031804.
XX PR 07-OCT-2002; 2002US-0416918P.
XX PA (Zymo ) ZYMOGENETICS INC.
XX PI Jaepers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
XX DR WPI; 2004-340913/31.
XX DR N-PSDB; ADN11755.
XX PT Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
XX PT inhibiting signal transduction in a cell expressing a growth hormone
XX PT secretagogue receptor, or treating a metabolic disorder.
XX PS Disclosure; Page 91-92; 100pp; English.
XX CC The present invention relates to the use of a zsig33 peptide for forming
XX CC a peptide-antibody complex, purifying a peptide, inhibiting signal
XX CC transduction in a cell expressing a growth hormone secretagogue receptor
XX CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
XX CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a
XX CC mammal, or treating a metabolic disorder. The peptide is useful for
XX CC forming a peptide-antibody complex, purifying a peptide, inhibiting
XX CC signal transduction in a cell expressing a GHS-R, decreasing fat
XX CC growth hormone secretion in pituitary cells of a mammal, or treating a
XX CC metabolic disorder. The zsig33 polypeptides can be used to study
XX CC proliferation or differentiation in stomach, lung, pituitary,
XX CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
XX CC skeletal muscle or pancreas. They are also useful in delivering
XX CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
XX CC also useful for promoting wound healing. The polypeptides, nucleic acids
XX CC and antibodies are useful for diagnosing, treating or preventing
XX CC disorders associated with gastric reflux, gastroparesis, modulation of
XX CC secretion of pituitary hormones, including growth hormone, Cohn's
XX CC disease, metabolic wasting, gastric ulcers, weight management, or
XX CC degenerative disease. The present sequence is the human GHS-R protein
XX SQ Sequence 366 AA;
Query Match 100.0%; Score 1905; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MWNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Db 1 MWNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Qy 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Db 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Qy 121 FVSESCYATVLTITALSVERVFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 180
Db 121 FVSESCYATVLTITALSVERVFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 180
Qy 181 LVGVEHENGTDPMWDTNECRPTFAVRSGLLTVMWVSSIFPFLPVFCLTVLYSLIGRKJL 240
Db 181 LVGVEHENGTDPMWDTNECRPTFAVRSGLLTVMWVSSIFPFLPVFCLTVLYSLIGRKJL 240
Qy 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Qy 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFEPPFSQKSLTLKDESSRAWT 360
Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFEPPFSQKSLTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366
```

Db 361 ESSINT 366

RESULT 11

ADO29025

ID ADO29025 standard; protein; 366 AA.

XX ADO29025;

AC ADO29025;

XX 29-JUL-2004 (first entry)

DT 29-JUL-2004 (first entry)

XX Human novel GPCR GHSR, SEQ ID NO:124.

XX

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;

KW transgenic mouse; neurological disorder; adrenal gland disorder;

KW colon disorder; intestinal disorder; cardiovascular disorder;

KW muscular disorder; blood disorder; immune disorder; bone disorder;

KW joint disorder; metabolic disorder; nutritive disorder; cancer;

KW kidney disorder; liver disorder; lung disorder; breast disorder;

KW ovary disorder; uterus disorder; prostate disorder; testis disorder;

KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;

KW thymus disorder; thyroid disorder; antiparkinsonian; antiarthritis;

KW cystostatic; antiinflammatory; vasotropic; antianginal; antidiabetic;

KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

KW viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;

KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;

KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;

KW receptor.

XX

XX Homo sapiens.

OS

XX WO2004040000-A2.

PN

XX 13-MAY-2004.

XX

XX 09-SEP-2003; 2003WO-US028226.

XX

XX 09-SEP-2002; 2002US-0409303P.

PR

XX 09-APR-2003; 2003US-0461329P.

XX

XX (PRIM-) PRIMAL INC.

PA

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, Meilwain KL, Pavlova MN, Vassiliadis D, Zeng H;

PI

XX WPI; 2004-390329/36.

DR N-PSDB; ADO29753.

XX

XX Novel mammalian G protein coupled receptors, useful for identifying

PT compounds that modulates diagnosing and treating disease condition

PT associated with GPCR dysfunction e.g. autoimmune diseases, angina

PT pectoris, Parkinson's disease.

XX

XX Claim 1; SEQ ID NO 124; 542pp; English.

PS

XX

XX The invention relates to human and mouse G protein-coupled receptors

CC (GPCRs) and nucleic acids encoding them. The invention also relates to

CC sequences at least 90% identical to the GPCR proteins and nucleic acids

CC of the invention; methods of treating, preventing or diagnosing diseases

CC associated with GPCRs of the invention; methods of screening for

CC compounds useful in the treatment of GPCR-related diseases; a transgenic

CC mouse comprising a GPCR gene of the invention; a mouse comprising a

CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived

CC from the transgenic mice; kits comprising several mice, each of which has

CC a mutation in a different GPCR gene of the invention; and kits comprising

CC probes which hybridize to GPCR polynucleotides of the invention. The

CC invention further discloses variants of the GPCR polypeptides and vectors

CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may

CC be used in the diagnosis, treatment or prevention of a wide variety of

CC diseases including neurological disorders (e.g., Alzheimer's disease,

CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);

CC disorders of the adrenal gland; disorders of the colon or intestine

CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel

CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or

CC myocardial infarction); muscular disorders; blood disorders (e.g.,

CC anaemia or leukaemia); immune disorders (e.g., osteoarthritis, rheumatoid

CC AIDS); bone and joint disorders (e.g., osteoporosis); metabolic disorders (e.g.,

CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,

CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related

CC diseases); and disorders of the kidney, liver, lung, breast, ovary,

CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and

CC thyroid (e.g., cancers). The present sequence represents a GPCR of the

CC invention. Note: The full sequence data for this patent did not form part

CC of the printed specification; those sequences not shown were obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

XX Sequence 366 AA;

SEQ

Query Match 100.0%; Score 1905; DB 8; Length 366;

Best Local Similarity 100.0%; Pred. No. 1.3e-200;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNATPSEPGFNLTLADLWDASPGNDSLGDELLOLPAPLLAGVTATCVLFFVVGAG 60

DB 1 MNATPSEPGFNLTLADLWDASPGNDSLGDELLOLPAPLLAGVTATCVLFFVVGAG 60

QY 61 NLLTMLVSVRRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQ 120

DB 61 NLLTMLVSVRRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQ 120

QY 121 FVSECTYATVLTITALSVERYFAICFFELRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180

DB 121 FVSECTYATVLTITALSVERYFAICFFELRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180

QY 181 LVGVEHGTDPWDTNECRPTFEFAVRSGLLTVMWVSSIFFELPVFCITLVLYSLGRKLM 240

DB 181 LVGVEHGTDPWDTNECRPTFEFAVRSGLLTVMWVSSIFFELPVFCITLVLYSLGRKLM 240

QY 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVVAFILCWLPHFVGRYLFKSFEPGSLIAQI 300

DB 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVVAFILCWLPHFVGRYLFKSFEPGSLIAQI 300

QY 301 SQYCNLVSFVLFYLSAANIPILYNIMSKYRVAVFRLIFGFPFPFSORKLSTLKDESSRAWT 360

DB 301 SQYCNLVSFVLFYLSAANIPILYNIMSKYRVAVFRLIFGFPFPFSORKLSTLKDESSRAWT 360

QY 361 ESSINT 366

DB 361 ESSINT 366

RESULT 12

ADQ28857

ID ADQ28857 standard; protein; 366 AA.

XX

XX ADQ28857;

XX

XX 23-SEP-2004 (first entry)

DT

XX Human ghrelin receptor amino acid sequence.

DE

XX human; ghrelin receptor; chromosome 3;

KW growth hormone secretagogue receptor isoform 1a;

KW motilin receptor homologue; ghrelin receptor inverse agonist;

KW eating-disorder; anorectic; analgesic; antianginal; antidiabetic;

KW antihypaemic; hypotensive; ghrelin receptor inhibitor;

KW hunger suppression; energy intake reduction; overeating; bulimia;

KW bulimia nervosa; obesity; Syndrome X; insulin resistance; dyslipidaemia;

KW impaired glucose tolerance; hypertension; Type II diabetes;

KW non insulin dependent diabetes mellitus; NIDDM.

XX

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH Disulfide-bond 116..198

FT

XX PN WO2004056869-A1.
 XX PD 08-JUL-2004.
 XX PF 20-DEC-2003; 2003WO-DK000924.
 XX PR 20-DEC-2002; 2002DK-00001983.
 XX PA (SEVE-) 7TM PHARMA AS.
 XX PI Lange BH, Schwartz TW, Frimurer TM, Rist O;
 XX DR WPI; 2004-525424/50.
 XX DR GENBANK; NP_940799.
 XX PT Novel inverse agonist of ghrelin receptor for medical use such as
 PT treatment or prophylaxis of feeding disorders including overeating e.g.,
 PT bulimia, bulimia nervosa, reduction of body weight, overweight, or
 PT obesity.
 XX PS Example 2; Fig 2; 61pp; English.
 XX CC The present invention describes an inverse agonist (I) of a ghrelin
 CC receptor for medical use. The ghrelin receptor is a motilin receptor
 CC homologue. Also described: (1) identifying (M1) (I), which involves
 CC contacting a ghrelin receptor with one or more test compounds without the
 CC presence of an agonist for the ghrelin receptor, measuring any change in
 CC the basal activity of the ghrelin receptor, and identifying test
 CC compounds that decreases the basal activity level of the ghrelin receptor
 CC with at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%,
 CC 70%, 75%, 80%, 85%, 90%, 95% or 100%; (2) preparing a pharmaceutical
 CC composition, which involves admixing (I) identified by (M1) with one or
 CC more excipients; and (3) a pharmaceutical composition (II) comprising (I)
 CC together with an excipient. (I) has eating-disorder, anorectic,
 CC analgesic, antianginal, antidiabetic, antilipaeamic and hypotensive
 CC activities, and can be used as a ghrelin receptor inhibitor. (I) is
 CC useful for modulating, by inverse agonism, the activity of a ghrelin
 CC receptor in a mammal. (I) is useful for the preparation of a composition
 CC for modifying the feeding behaviour of a mammal including a human, such
 CC as suppressing hunger or reducing energy intake, or for the treatment or
 CC prophylaxis of feeding disorders including overeating e.g., bulimia,
 CC bulimia nervosa, reduction of body weight, overweight, and/or obesity,
 CC Syndrome X (metabolic syndrome) or any combination of obesity, insulin
 CC resistance, dyslipidaemia, impaired glucose tolerance and hypertension,
 CC Type II diabetes or non insulin dependent diabetes mellitus (NIDDM) or
 CC its complications. The present sequence represents the human ghrelin
 CC receptor amino acid sequence, which is used in the exemplification of the
 CC present invention. The human ghrelin receptor gene is located on
 CC chromosome 3, more specifically to 3q26.31. The human ghrelin receptor is
 CC also known as the growth hormone secretagogue receptor isoform 1a (see
 CC Genbank NP_940799).
 XX SQ Sequence 366 AA;

Query Match
 Best Local Similarity 100.0%; Score 1905; DB 8; Length 366;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWNATPSEEPGNLTADLDWDASFGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
 Db 1 MWNATPSEEPGNLTADLDWDASFGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
 Qy 61 NLLTMLVVSREPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
 Db 61 NLLTMLVVSREPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
 Qy 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGPIFV 180
 Db 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGPIFV 180
 Qy 181 LVGVEHNGTDPWDTNCRPTFEAVRSGLLTVMVWVSSIFFLPVCLTVLYSLIGRKLW 240
 Db 181 LVGVEHNGTDPWDTNCRPTFEAVRSGLLTVMVWVSSIFFLPVCLTVLYSLIGRKLW 240

Db 181 LVGVEHNGTDPWDTNCRPTFEAVRSGLLTVMVWVSSIFFLPVCLTVLYSLIGRKLW 240
 Qy 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAFICLWLPFHVGRYLFKSPFPGSLIEIAQI 300
 Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAFICLWLPFHVGRYLFKSPFPGSLIEIAQI 300
 Qy 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFPFPFSQKSLSTLKDESSRAWT 360
 Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFPFPFSQKSLSTLKDESSRAWT 360
 Qy 361 ESSINT 366
 Db 361 ESSINT 366
 RESULT 13
 RAY90666
 ID AAY90666 standard; protein; 366 AA.
 XX AC AAY90666;
 XX DT 21-AUG-2000 (first entry)
 XX DE Human mutant G protein-coupled receptor GHSR (V262K).
 XX KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
 KW antagonist; mutant; mutain.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200022129-A1.
 XX PD 20-APR-2000.
 XX PF 12-OCT-1999; 99WO-US023938.
 XX PR 13-OCT-1998; 98US-00170496.
 XX PA (AREN-) ARENA PHARM INC.
 XX PI Behan DP, Chalmers DT, Liaw CW;
 XX WPI; 2000-329165/28.
 XX N-PSDB; AAA30732.
 XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents.
 PS Example 2; Page 267-268; 341pp; English.
 CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
 CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
 CC and AAA30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
 CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of

CC compounds without the need for endogenous ligands. Sequences AAY90643-
 CC AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention
 XX
 SQ Sequence 366 AA;

Query Match 99.7%; Score 1899; DB 3; Length 366;
 Best Local Similarity 99.7%; Pred. No. 6.1e-200;
 Matches 365; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNATPSEEPGNLTADLDWDASPGNDSLGDELLQFPAPLAGVTATCVAFVVGAG 60
 DB 1 MNATPSEEPGNLTADLDWDASPGNDSLGDELLQFPAPLAGVTATCVAFVVGAG 60

QY 61 NLLTMLVSVRFRELTNTNLYLSSMAFSDLLIFLCMPDLVLWQYRPNWFGDLCKLFQ 120
 DB 61 NLLTMLVSVRFRELTNTNLYLSSMAFSDLLIFLCMPDLVLWQYRPNWFGDLCKLFQ 120

QY 121 FVSECTYATVLTITALSVERVFAICFPLRAKVVTKGRVKLVIVWAVAFCSAGPIFV 180
 DB 121 FVSECTYATVLTITALSVERVFAICFPLRAKVVTKGRVKLVIVWAVAFCSAGPIFV 180

QY 181 LVGVEHGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLYSLGRKLM 240
 DB 181 LVGVEHGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLYSLGRKLM 240

QY 241 RRRRGDAVVGASLRDNHKTVMKLVAVVFAFICLWLPFHVGRYLFKSFEPGSLEIAQI 300
 DB 241 RRRRGDAVVGASLRDNHKTVMKLVAVVFAFICLWLPFHVGRYLFKSFEPGSLEIAQI 300

QY 301 SOYCNLVSVFLYLSAANPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360
 DB 301 SOYCNLVSVFLYLSAANPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360

QY 361 ESSINT 366
 DB 361 ESSINT 366

RESULT 14
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 ID ADC22729 standard; protein; 366 AA.
 XX
 AC ADC22729;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human G protein-coupled receptor (GPCR) polypeptide #63.
 XX
 KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
 KW intracellular-3 region; IC3; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US6555339-B1.
 XX
 PD 29-APR-2003.
 XX
 PF 13-OCT-1998; 98US-00170496.
 XX
 PR 14-APR-1997; 97US-00839449.
 PR 14-APR-1998; 98US-00060188.
 PR 26-JUN-1998; 98US-0090783P.
 PR 07-AUG-1998; 98US-0095677P.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Liaw CW, Behan DP, Chalmers DT;
 XX
 XX WPI; 2003-742861/70.
 DR N-PSDB; ADC22728.
 XX
 PT Creating a constitutively active version of an endogenous human G protein
 PT coupled receptor (GPCR) comprises substituting a specific amino acid in

PT the transmembrane-6 region with a different amino acid, and testing for
 PT constitutive activity.
 XX
 PS Example 2; SEQ ID NO 210; 221pp; English.
 XX
 CC The invention relates to a method for treating a non-endogenous,
 CC constitutively active version of an endogenous human G protein-coupled
 CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an
 CC intracellular-3 (IC3) region, by substituting a specific amino acid in
 CC the TM6 region with a different amino acid, and testing for constitutive
 CC activity. The method is useful for creating a constitutively active
 CC version of an endogenous human GPCR that comprises a transmembrane 6
 CC region and an intracellular loop 3 region. The altered human GPCR
 CC polypeptides are useful for screening test compounds for identification
 CC of inverse agonists or partial agonists of GPCR polypeptides, which may
 CC have therapeutic uses. The altered GPCRs may also be used in vivo or in
 CC vitro in biological research. A nucleic acid encoding the altered GPCR
 CC may be used to create a transgenic animal expressing the altered GPCR.
 CC The method allows screening for compounds that modulate the activity of a
 CC human G protein-coupled receptor without the need for provision of a
 CC ligand for the receptor. This is particularly useful in allowing
 CC screening of compounds against orphan receptors for which no ligand is
 CC currently known. This sequence represents a human GPCR polypeptide of the
 CC invention.

SQ Sequence 366 AA;

Query Match 99.7%; Score 1899; DB 7; Length 366;
 Best Local Similarity 99.7%; Pred. No. 6.1e-200;
 Matches 365; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 FVSECTYATVLTITALSVERVFAICFPLRAKVVTKGRVKLVIVWAVAFCSAGPIFV 180
 DB 121 FVSECTYATVLTITALSVERVFAICFPLRAKVVTKGRVKLVIVWAVAFCSAGPIFV 180

QY 181 LVGVEHGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLYSLGRKLM 240
 DB 181 LVGVEHGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLYSLGRKLM 240

QY 241 RRRRGDAVVGASLRDNHKTVMKLVAVVFAFICLWLPFHVGRYLFKSFEPGSLEIAQI 300
 DB 241 RRRRGDAVVGASLRDNHKTVMKLVAVVFAFICLWLPFHVGRYLFKSFEPGSLEIAQI 300

QY 301 SOYCNLVSVFLYLSAANPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360
 DB 301 SOYCNLVSVFLYLSAANPILYNIMSKKYRVAVFRLGFEFPFSQKSLSTLKDESSRAWT 360

QY 361 ESSINT 366
 DB 361 ESSINT 366

RESULT 15
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 ID ADH14202 standard; protein; 366 AA.
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 AC ADH14202;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Mutated human GHSR.
 XX
 KW human; non-endogenous; G protein-coupled receptor; GPCR; receptor;
 KW mutant; mutein.
 XX

Search completed: April 10, 2006, 17:28:40
Job time : 208.354 secs

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OS Synthetic.
OS Homo sapiens.
XX US2003105292-A1.
XX
XX 05-JUN-2003.
XX
XX 20-SEP-2002; 2002US-00251385.
XX
XX 26-JUN-1998; 98US-0090783P.
XX 07-AUG-1998; 98US-0095677P.
XX 13-OCT-1998; 98US-00170496.
XX
XX (LIAW/) LIAW C W.
XX (BEHA/) BEHAN D P.
XX (CHAL/) CHALMERS D T.
XX
XX Liaw CW, Behan DP, Chalmers DT;
XX
XX WPI; 2003-801247/75.
XX N-PSDB; ADH14201.
XX
XX New constitutively active, non-endogenous version of an endogenous human
XX G protein-coupled receptor for the identification of therapeutic
XX compounds, such as agonists.
XX
XX Example 2; SEQ ID NO 210; 227pp; English.
XX
XX The invention relates to a constitutively active, non-endogenous version
XX of an endogenous human G protein-coupled receptor (GPCR). The GPCR is
XX used for screening therapeutic compounds as inverse agonists, agonists or
XX partial agonists. The GPCR can be also be used to elucidate and
XX understand the roles of GPCRs in normal and diseased humans. The GPCR
XX need not be purified and isolated to be used to screen for therapeutic
XX compounds. The utility of the GPCR as a research tool is enhanced because
XX the role of a particular receptor can be understood before the endogenous
XX ligand is identified. The present sequence is used in the exemplification
XX of the present invention.
XX
XX Sequence 366 AA;
XX
Query Match 99.7%; Score 1899; DB 7; Length 366;
Best Local Similarity 99.7%; Pred. No. 6.1e-200;
Matches 365; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVLFVVGIAG 60
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Db 181 LVGVHEHNGTDPMDTNECRPTEFAVRSGLLTVMWVSSIFFEFLPVCLTVLYSLIGRKLW 240
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Db 241 RRRGDAVVGASLRDQNHKQTKMLAVVVFATILCMLPFHVGRYLFKSPFGSLLEIAQI 300
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Db 301 SQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLLGPEPFSQRKSLTKDESSRAWT 360
QY 361 ESSINT 366
Db 361 ESSINT 366
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:33:53 ; Search time 51.528 Seconds
(without alignments)
587.240 Million cell updates/sec

Title: US-09-718-803A-5
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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1905	100.0	366	2	US-09-077-675A-13
2	1905	100.0	366	2	US-09-077-674-13
3	1905	100.0	366	2	US-09-170-496D-88
4	1905	100.0	366	2	US-09-743-742B-7
5	1905	100.0	366	2	US-09-762-661A-5
6	1905	100.0	366	2	US-09-364-425B-45
7	1905	100.0	366	2	US-09-743-475-4
8	1899	99.7	366	2	US-09-170-496D-210
9	1874	98.4	361	2	US-09-077-675A-8
10	1874	98.4	361	2	US-09-077-674-8
11	1789	93.9	364	2	US-09-077-675A-16
12	1789	93.9	364	2	US-09-077-674-16
13	1789	93.9	364	2	US-09-762-661A-6
14	1789	93.9	364	2	US-09-743-475-5
15	1788	93.9	364	2	US-09-743-475-3
16	1771	93.0	366	2	US-09-762-661A-7
17	1771	93.0	366	2	US-09-743-475-6
18	1704	89.4	353	2	US-09-077-675A-3
19	1704	89.4	353	2	US-09-077-674-3
20	1596.5	83.8	349	2	US-09-762-661A-2
21	1569	82.4	302	2	US-09-077-675A-7
22	1569	82.4	302	2	US-09-077-674-7
23	1493	78.4	302	2	US-09-077-675A-2
24	1493	78.4	302	2	US-09-077-674-2
25	1418	74.4	271	2	US-09-077-675A-12
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Sequence 10, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 535, App
Sequence 114, Appl
Sequence 4, Appl
Sequence 10, Appl
Sequence 224, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 10101, A
Sequence 12, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 45, Appl

28 1388 72.9 289 2 US-09-077-674-10
29 1258 66.0 289 2 US-09-077-675A-5
30 1258 66.0 289 2 US-09-077-674-5
31 863.5 45.3 412 2 US-09-743-742B-8
32 460 24.1 418 2 US-09-743-742B-5
33 454 23.8 418 2 US-09-826-509-535
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37 450.5 23.6 403 2 US-09-170-496D-224
38 446 23.4 415 2 US-09-341-016A-1
39 445 23.4 415 2 US-09-545-944-2
40 445 23.4 415 2 US-10-215-619-2
41 444 23.3 412 2 US-09-949-016-10101
42 444 23.3 415 2 US-09-875-076-12
43 442 23.2 405 2 US-09-743-742B-2
44 442 23.2 405 2 US-09-743-742B-11
45 420.5 22.1 353 1 US-08-118-270-45

ALIGNMENTS

RESULT 1
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; Sequence 13, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-13

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Best Local Similarity 100.0%; Pred. No. 1.8e-154;

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Db	61	NLLTMLVVSFRPRELRTTNLYLSNMAFSDDLIFLCMPDLVLRLWQYRPWNFGDLLCKL	120						
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Qy	181	LVGVEHENGTDPMWDTNECRPTFAVRSGLLTVMVVSSIFFFLPVFCLTVLYSLIGRKLW	240						
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Qy	301	SOYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLLGPPFPFQORKLSTLKDESSRAWT	360						
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RESULT 2

97,21736

US-09-077-674-13
Sequence 13, Application US/09077674
Patent No. 6531314
GENERAL INFORMATION:
APPLICANT: Atena, Joseph P.
APPLICANT: Cully, Doris F.
APPLICANT: Feighner, Scott D.
APPLICANT: Howard, Andrew D.
APPLICANT: Liberator, Paul A.
APPLICANT: Schaeffer, James M.
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,674
FILING DATE: 3-JUN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19589P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 13:

97,21736

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 366 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-09-077-674-13

Query Match          100.0%; Score 1905; DB 2; Length 366;
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Qy  121  FVSESCYATVLTITALTALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGIFV 180
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Qy  181  LVGVEHNGTDPMDTNECRTEPAVRSGLITVMWVSSIFFFLPVFCLTVLYSLIGRKLW 240
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Qy  361  ESSINT 366
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Db   361  ESSINT 366
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RESULT 3
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; Sequence 88, Application US/09170496D
; Patent No. 6553339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-170-496D-88

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; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Chen, Ruoping
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
; FILE REFERENCE: Are0047
; CURRENT APPLICATION NUMBER: US/09/364,425B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/094,879
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/106,300
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/110,906
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-364-425B-45

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RESULT 7
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; Sequence 4, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10

; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Chen, Ruoping
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
; FILE REFERENCE: Are0047
; CURRENT APPLICATION NUMBER: US/09/364,425B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/094,879
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/106,300
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/110,906
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-364-425B-45

Query Match          100.0%; Score 1905; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.8e-154; Indels 0; Gaps 0;
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QY 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAG 60
Db 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAG 60

QY 61 NLLTMLVSVRPRELRTTNLYLSSMAFSDLLIFLCMPDLVLRLQYRPWNFGDLLCKLFQ 120
Db 61 NLLTMLVSVRPRELRTTNLYLSSMAFSDLLIFLCMPDLVLRLQYRPWNFGDLLCKLFQ 120

QY 121 FVSECTVATVTITALSVERYFAICPLRAKVVTKGRVKLVFVIWAVAFCSAGPIFV 180
Db 121 FVSECTVATVTITALSVERYFAICPLRAKVVTKGRVKLVFVIWAVAFCSAGPIFV 180

QY 181 LVGVEHNGTDPWDNECRPTFEFVRSGLLTVWVWSIFFPFLPVFCLTVLYSLIGRKLW 240
Db 181 LVGVEHNGTDPWDNECRPTFEFVRSGLLTVWVWSIFFPFLPVFCLTVLYSLIGRKLW 240

QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEPGSLLEIAQI 300
Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEPGSLLEIAQI 300

QY 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLLGFEPFSORKLSTLKDESSRAWT 360
Db 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLLGFEPFSORKLSTLKDESSRAWT 360

QY 361 ESSINT 366
Db 361 ESSINT 366

RESULT 8
US-09-170-496D-210
; Sequence 210, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 210
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-210

Query Match          99.7%; Score 1899; DB 2; Length 366;
Best Local Similarity 99.7%; Pred. No. 5.8e-154; Indels 0; Gaps 0;
Matches 365; Conservative 0; Mismatches 1;

QY 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAG 60
Db 1 MNATPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAG 60
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QY 61 NLLTMLVSRRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
DB 61 NLLTMLVSRRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
QY 121 FVSECTATVLTITALSVERFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTATVLTITALSVERFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFV 180
QY 181 LVGEHENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCITVLYSLIGRKLW 240
DB 181 LVGEHENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCITVLYSLIGRKLW 240
QY 241 RRRGDAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIAQI 300
DB 241 RRRGDAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIAQI 300
QY 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLGPFPSQKSLTKDESSRAWT 360
DB 301 SOYCNLVSVFLYLSAAINPILYNIMSKKYRVAVFRLGPFPSQKSLTKDESSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366

RESULT 9
US-09-077-675A-8
; Sequence 8, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-8

Query Match 98.4%; Score 1874; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.7e-152;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PSEBPGFNLTADLDWDASPGNDSIGDELLQLFPAPLLAGVTATCVALFVVGIAGNLLTM 65
DB 1 PSEBPGFNLTADLDWDASPGNDSIGDELLQLFPAPLLAGVTATCVALFVVGIAGNLLTM 60
QY 66 LVSRFRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSES 125
DB 61 LVSRFRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSES 120
QY 126 CTYATVLTITALSVERFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFVVLVGE 185
DB 121 CTYATVLTITALSVERFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFVVLVGE 180
QY 186 HENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCITVLYSLIGRKLWRRRG 245
DB 181 HENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCITVLYSLIGRKLWRRRG 240
QY 246 DAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIAQISOYCN 305
DB 241 DAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIAQISOYCN 300
QY 306 LVSPVLFYLSAAINPILYNIMSKKYRVAVFRLGPFPSQKSLTKDESSRAWTESSIN 365
DB 301 LVSPVLFYLSAAINPILYNIMSKKYRVAVFRLGPFPSQKSLTKDESSRAWTESSIN 360
QY 366 T 366
DB 361 T 361
RESULT 10
US-09-077-674-8
; Sequence 8, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273

```
;
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-674-8

Query Match      98.4%; Score 1874; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.7e-152;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIGNLLTM 65
Db 1 PSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIGNLLTM 60

QY 66 LVVSFRFRLTTNNLYLSSMAFSDLLIFLCWPLDLVRLWQYRPNWFGDLCKLQFVSES 125
Db 61 LVVSFRFRLTTNNLYLSSMAFSDLLIFLCWPLDLVRLWQYRPNWFGDLCKLQFVSES 120

QY 126 CTYATVLTITALSVERFYFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFVLVGV 185
Db 121 CTYATVLTITALSVERFYFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFVLVGV 180

QY 186 HENGTDPMWTECRTEFAVRSGLLTVMVWSSIFFFLPVFCCLTVLYSLIGRKLWRRRG 245
Db 181 HENGTDPMWTECRTEFAVRSGLLTVMVWSSIFFFLPVFCCLTVLYSLIGRKLWRRRG 240

QY 246 DAVGASLRDQNHKQTVKMLAVVVFATILCWLPHFVGRVLYFSKSPESGLETAQISQYCN 305
Db 241 DAVGASLRDQNHKQTVKMLAVVVFATILCWLPHFVGRVLYFSKSPESGLETAQISQYCN 300

QY 306 LVSFVFLYLSAAINPILYNIMSKKYRVAVFRLLGPEFVSQKSLSTLKDESSRAWTESSIN 365
Db 301 LVSFVFLYLSAAINPILYNIMSKKYRVAVFRLLGPEFVSQKSLSTLKDESSRAWTESSIN 360

QY 366 T 366
Db 361 T 361

RESULT 11
US-09-077-675A-16
; Sequence 16, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

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;
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-16

Query Match      93.9%; Score 1789; DB 2; Length 364;
Best Local Similarity 95.6%; Pred. No. 1.4e-144;
Matches 350; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

QY 1 MNWATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 60
Db 1 MNWATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 59

QY 61 NLLTMLVSVRPRELRTTNLYLSSMAFSDLLIFLCWPLDLVRLWQYRPNWFGDLCKLQ 120
Db 60 NLLTMLVSVRPRELRTTNLYLSSMAFSDLLIFLCWPLDLVRLWQYRPNWFGDLCKLQ 119

QY 121 FVSSCTVATVLTITALSVERFYFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 180
Db 120 FVSSCTVATVLTITALSVERFYFAICFPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 179

QY 181 LVGVEHENGTDPMWTECRTEFAVRSGLLTVMVWSSIFFFLPVFCCLTVLYSLIGRKLW 240
Db 180 LVGVEHENGTDPMWTECRTEFAVRSGLLTVMVWSSIFFFLPVFCCLTVLYSLIGRKLW 239

QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFATILCWLPHFVGRVLYFSKSPESGLEIAQI 300
Db 240 -RRRGDAVVGASLRDQNHKQTVKMLAVVVFATILCWLPHFVGRVLYFSKSPESGLEIAQI 298

QY 301 SOYCNLYSFVLYLSAAINPILYNIMSKKYRVAVFRLLGPEFVSQKSLSTLKDESSRAWT 360
Db 299 SOYCNLYSFVLYLSAAINPILYNIMSKKYRVAVFRLLGPEFVSQKSLSTLKDESSRAWT 358

QY 361 ESSINT 366
Db 359 KSSINT 364

RESULT 12
US-09-077-674-86
; Sequence 16, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
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COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-SEQ for Windows Version 2.0
 CURRENT APPLICATION DATA: US/09/077,674
 FILING DATE: 3-JUN-1998
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cocuzzo, Anna L.
 REGISTRATION NUMBER: 42,452
 REFERENCE/DOCKET NUMBER: 19589P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 732-594-1273
 TELEFAX: 732-594-4720
 TELEX:
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-077-674-16

Query Match 93.9%; Score 1789; DB 2; Length 364;
 Best Local Similarity 95.6%; Pred. No. 1.4e-144;
 Matches 350; Conservative 5; Mismatches 9; Indels 2; Gaps 2;
 QY 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG 60
 DB 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG 59
 QY 61 NLLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQ 120
 DB 60 NLLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQ 119
 QY 121 FVSESCYATVLTITALSVERYFAICPPLRAKVVTGRVKLVIFVWAVAFCSAGPIFV 180
 DB 120 FVSESCYATVLTITALSVERYFAICPPLRAKVVTGRVKLVIFVWAVAFCSAGPIFV 179
 QY 181 LVGVEHNGTDPWDTNCRPTFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 240
 DB 180 LVGVEHNGTDPWDTNCRPTFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 239
 QY 241 RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPEPGSLEIAQI 300
 DB 240 -RRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPEPGSLEIAQI 298
 QY 301 SOYCNLVSVFVLYLSAIPILYNIMSKYRVAVRLLGLPEPFSQKSLTKDESSRAWT 360
 DB 299 SOYCNLVSVFVLYLSAIPILYNIMSKYRVAVRLLGLPEPFSQKSLTKDESSRAWT 358
 QY 361 ESSINT 366
 DB 359 KSSINT 364

RESULT 13
 US-09-762-661A-6
 ; Sequence 6, Application US/09762661A
 ; Patent No. 6645726
 ; GENERAL INFORMATION:
 ; APPLICANT: Howard, Andrew D.
 ; APPLICANT: Palyha, Oksana C.
 ; APPLICANT: Smith, Roy G.
 ; APPLICANT: Tan, Carina P.
 ; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
 ; TITLE OF INVENTION: RECEPTOR

FILE REFERENCE: 20207P
 CURRENT APPLICATION NUMBER: US/09/762,661A
 CURRENT FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: PCT/US99/17915
 PRIOR FILING DATE: 1999-08-06
 PRIOR APPLICATION NUMBER: 60/095,960
 PRIOR FILING DATE: 1998-08-10
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 364
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-09-762-661A-6

Query Match 93.9%; Score 1789; DB 2; Length 364;
 Best Local Similarity 95.6%; Pred. No. 1.4e-144;
 Matches 350; Conservative 5; Mismatches 9; Indels 2; Gaps 2;
 QY 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG 60
 DB 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG 59
 QY 61 NLLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQ 120
 DB 60 NLLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDILCKLFQ 119
 QY 121 FVSESCYATVLTITALSVERYFAICPPLRAKVVTGRVKLVIFVWAVAFCSAGPIFV 180
 DB 120 FVSESCYATVLTITALSVERYFAICPPLRAKVVTGRVKLVIFVWAVAFCSAGPIFV 179
 QY 181 LVGVEHNGTDPWDTNCRPTFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 240
 DB 180 LVGVEHNGTDPWDTNCRPTFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 239
 QY 241 RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPEPGSLEIAQI 300
 DB 240 -RRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPEPGSLEIAQI 298
 QY 301 SOYCNLVSVFVLYLSAIPILYNIMSKYRVAVRLLGLPEPFSQKSLTKDESSRAWT 360
 DB 299 SOYCNLVSVFVLYLSAIPILYNIMSKYRVAVRLLGLPEPFSQKSLTKDESSRAWT 358
 QY 361 ESSINT 366
 DB 359 KSSINT 364

RESULT 14
 US-09-743-475-5
 ; Sequence 5, Application US/09743475
 ; Patent No. 6682908
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Roy G.
 ; APPLICANT: Van der Ploeg, Leonardus H. T.
 ; APPLICANT: Howard, Andrew D.
 ; APPLICANT: Zheng, Hui
 ; APPLICANT: McKee, Karen Kulju
 ; APPLICANT: Jiang, Michael M.
 ; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
 ; FILE REFERENCE: 20218P
 ; CURRENT APPLICATION NUMBER: US/09/743,475
 ; CURRENT FILING DATE: 2001-01-10
 ; PRIOR APPLICATION NUMBER: PCT/US99/15375
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: 60/092,361
 ; PRIOR FILING DATE: 1998-07-10
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 364
 ; TYPE: PRT

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; ORGANISM: Rattus norvegicus
US-09-743-475-5

Query Match      93.9%; Score 1789; DB 2; Length 364;
Best Local Similarity 95.6%; Pred. No. 1.4e-144;
Matches 350; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

QY 1 MNATPSEPGNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNATPSEPEPNVTL-DLDWDASPGNDSLDPELLPLPAPLLAGVTATCVAFVVGISG 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NLLTMLVVSRRFRELRTTNLYLSSNAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 NLLTMLVVSRRFRELRTTNLYLSSNAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LVGVEHENGTDPDWTDNECRPTPEFAVRSGLLTVMWVSSIFPFLPVFCLTVLYSLIGRKLW 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 LVGVEHENGTDPRDTPNECRATEFAVRSGLLTVMWVSSVFFFLPVFCLTVLYSLIGRKLW 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSFPFGSLEIAQI 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 -RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSFPFGSLEIAQI 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 SOYCNLVSFVLYLSAAINPILYNIMSKKYRVAVFRLLGPFPPFSQORKLSTLKDESSRAWT 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 SOYCNLVSFVLYLSAAINPILYNIMSKKYRVAVFRLLGPFPPFSQORKLSTLKDESSRAWT 358
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 361 ESSINT 366
   :|||||
Db 359 KSSINT 364
   :|||||
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Search completed: April 10, 2006, 17:35:43
Job time : 52.528 secs

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RESULT 15
US-09-743-475-3
; Sequence 3, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-743-475-3

Query Match      93.9%; Score 1788; DB 2; Length 364;
Best Local Similarity 95.4%; Pred. No. 1.7e-144;
Matches 349; Conservative 6; Mismatches 9; Indels 2; Gaps 2;

QY 1 MNATPSEPGNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MNATPSEPEPNVTL-DLDWDASPGNDSLSDELLPLPAPLLAGVTATCVAFVVGISG 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NLLTMLVVSRRFRELRTTNLYLSSNAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 120
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